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OM protein - protein search, using sw model

Run on: September 30, 2002, 14:59:19 ; Search time 41.9 Seconds  
 (without alignments)  
 3719.249 Million cell updates/sec

Title: US-09-830-338-1

Searched: Perfect score: 7308

Sequence: 1 MATQOKASDERISQFDHNLL.....SKYLTILQKWLIPFSPPIQK 1403

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Database : A\_Geneseq\_032802:\*

1: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1980.DAT:\*

2: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1983.DAT:\*

5: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1984.DAT:\*

6: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1985.DAT:\*

7: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1986.DAT:\*

8: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1987.DAT:\*

9: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1988.DAT:\*

10: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1990.DAT:\*

11: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1991.DAT:\*

12: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1992.DAT:\*

13: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1993.DAT:\*

14: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1994.DAT:\*

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16: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1996.DAT:\*

17: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1997.DAT:\*

18: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1998.DAT:\*

19: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA1999.DAT:\*

20: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA2000.DAT:\*

21: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

22: /SIDS1/gcadata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	7308	100.0	1403	18 AAW20032
2	7308	100.0	1403	20 AAY1079
3	7308	100.0	1403	20 AAY09539
4	100.0	1403	21	AAY88053
5	7284	99.7	1403	18 AAW20033
6	6691	91.6	1295	20 AAY14080
7	6691	91.6	1295	20 AAY09540
8	6373.5	87.2	1232	17 AAR98217
9	661	9.0	1204	22 AAU02881
10	654	8.9	1070	22 AAG6752
11	653	8.9	1024	22 AAU02880

RESULT 1

ID AAW20032 standard; Protein: 1403 AA.

XX AAW20032;

XX DT 06-OCT-1997 (first entry)

XX DE Neuronal apoptosis inhibitor protein (NAIP).

XX KW Neuronal apoptosis inhibitor protein; NAIP; diagnosis; KW therapy; cancer; AIDS; amyotrophic lateral sclerosis; KW spinal muscular atrophy.

XX OS Homo sapiens.

XX PN W09726331-A2.

XX PD 24-JUL-1997. (V?)

XX PR 17-JAN-1997; 97W0-LB00142.

XX PR 19-JAN-1996; 96GB-0001108.

XX PA (UYOT) UNIV OTTAWA.

XX PI Korneluk RG, Mackenzie AE, Robertson G, Roy N, Tamai K;

XX DR WPI; 1997-385335/35.

XX DR N-PSDB; AAT71205.

XX PT New neuronal inhibitor of apoptosis - useful for diagnosing and PT treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis

XX Human caspase recr

Murine ESM encoded Human colon cancer

Amino acid sequenc Human inhibitor of Human apoptosis in Human c-AP1. Hom Human HTRP-2 Prote Human cellular inh Murine c-AP1. Murine HTRP-2 prot Murine apoptosis in Murine HTRP-1 Prot Murine apoptosis in Mouse inhibitor of Human inhibitor of Human c-AP2. Hom Human cellular inh Human XIPR protein Human apoptosis in Human XIAP protein Human k-linked inh Human protein seq Human inhibitor of Drosophila melanog Drosophila inhibit Human secreted pro Angiotensin conver Drosophila mutant

PS	Claim 41; Fig 6A-I; 102pp; English.
XX	
CC	Novel human neuronal apoptosis inhibitor protein (AAW20037), or NATP,
CC	is a negative regulator of apoptosis, partic. neuronal apoptosis
CC	and, when deficient or absent, contributes to neurodegenerative
CC	phenotypes such as spinal muscular atrophy (SMA) and amyotrophic
CC	lateral sclerosis. Its amino acid sequence was deduced from a
CC	library. NATP polypeptides, esp. those containing at least two
CC	BIR (baculovirus IAP repeat) domains, can be expressed in host-
CC	treatment of AIs, neurodegenerative disease, myelosympathic
CC	syndromes or ischaemic injury, to screen for (ant)agonists, or to
XX	produce antibodies useful for inhibiting apoptosis.
SQ	Sequence 1403 AA:
	Query Match
	best local Similarity 100.0%; Score 7308; DB 18; Length 1403;
	Matches 1403; Conservative 0; Pred. No. 0; Mismatches 0; Gaps 0;
QY	1 MATOOKASDERRISOFDHNLPELPSALLGDAVOLAKELEEEQERAKKQKGINSQRMSE 60
Db	1 matogkanderiegfdhnlpealsalglgdaqvlakleeeerkerakmgkgynsqmse 60
QY	61 AKRLKTFETYEPYESSWTRPQEMAMAGSYFTGKGSGIQCFCSTLFLGQLRIPIEDHKF 120
Db	61 akrikftfetyepyesswtpqemanaadgfyfgksgiqfcscallfagqltripehdhf 120
QY	121 HPGCGFLINKDGNIKYKD1RKNUKSURGGKARYQEEARLASEFENNPYVGSPCV 180
Db	121 hpdgflinkgvgnakdydikvknksrigmryqeeearlasfnnwpyvgspcv 180
QY	181 LSEAGEVFTGHQDTYOCFSGCCGCGNWERGDDEWKEAHKWFPECELTRSKKSSEITQYI 240
Db	181 lsagavftgkqdtvqcfscggcgcgnwgewdpwkelnkwipkefirsksseitqy 240
QY	241 QSYKGRVDITGEHVNMSWQRETFPMASACYCNDSIFAAVEELRDLSDFKDWRESAVVAALA 300
Db	241 qsykgrvditgehvnmswqretpfmasyacysifaaeirlsdwdpresaavaala 300
QY	301 KAGARYTGKDIYQCFSGGCLEKWKOBGDDPLDHDHRCFFNCPIQNMMSSAETVTPDQS 360
Db	301 kagaytgkdiyqcfscggcgcgnwgewdpwkelnkwipkefirsksseitqy 360
QY	361 RGLCILELTTESSENLDSIAVGPVPEMAQENOWFOEAKNNEOLRAYASAERHMS 420
Db	361 rgliclelttessnledsavgpvpemaqeqowfqeaknneolrayasaerhms 420
QY	421 LUDLISSOLATHLGLDLSASKHSKPYQEPVLPVEFGNUNSVMOVEGAGSCKTLL 480
Db	421 luidssolatdhlgldslaskhskpyqepvlpvefgnunsvmegeagscktl 480
QY	481 KKLAFIWAASGCCPLNRFOLVFYSLSSTRPBG LASICPOLLEKEGYTEMCRNITQ 540
Db	481 kklatwasgccplnrfgvfvlslsstipoglasicqklegsysystemcnitq 540
QY	541 OLKNOVLFULLDVKREICSTPOVIGKLQKHNLSRCLLIVRTNRHARDTRYLETILIRK 600
Db	541 qklnqvfllddkreicsipqvgikqknlsrltcillaavrtdardirvyleik 600
QY	601 AFPYNTVCLRLFLSHMTRLKMYFGNOSIKIOTPLWVATCAHWQYRPDP 660
Db	601 afpnyntvcilrlflshmtrlkfnyqkngsqkqktpfvaalcahufqyfpds 660
QY	661 FPDVAVFSYMERLISRKNATAEKATVSSCGELALGGFSCCFERNDOLAEAVDED 720
Db	661 fdavavfsymerlirkataekatvsscgelalggfscfendaldaevded 720
QY	721 EPLTMCLMSKTAQRLRPFRLSPAFQFLAGMRLLBLSDRQMDGGLYHJKQNS 780
Db	721 edtlmclmsktaqrlrpfrlspafqflagmrllbdrgengdighlyhjkqns 780
DR	
DR	RESULT 2
	AYA14079
	ID AY14079 standard; Protein; 1403 AA.
	XX
	AC AY14079;
	XX
	DT 20-JUL-1999 (first entry)
	XX
	DE Gonadotropin
	XX
	Conadotropin hormone protein sequence.
	KW Gonadotropin hormone; excessive ovulation animal; transgenic animal;
	KW totipotent cell; somatic cell chromosome.
	OS Homo sapiens.
	XX
	PN JPI11344-A.
	XX
	KW Gonadotropin hormone; excessive ovulation animal; transgenic animal;
	XX
	PR 14-OCT-1997; 97JP-0280830.
	XX
	PR 14-OCT-1997; 97JP-0280830.
	XX
	PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
	PA (SAKA-) SAKAI H.
	XX
DR	WPI; 1999-320709/27.

Om protein - protein search, using sw model						
Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5					
Scoring table:	BLOSUM62					
Searched:	105224 seqs, 38719550 residues					
Total number of hits satisfying chosen parameters:	105224					
Minimum DB seq length: 0						
Maximum DB seq length: 200000000						
Post-processing: Minimum Match 0%						
Post-processing: Maximum Match 100%						
Database :	Swissprot_40;*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	RESULT 1
1	7308	100.0	1403	1	BIRL_HUMAN	BIRL_HUMAN STANDARD; PRT: 1403 AA.
2	4956	67.8	1403	1	BIRL_MOUSE	ID=BIRL_HUMAN Q13075; 013730; 099796; 075857;
3	4919	67.3	1447	1	BIRB_MOUSE	DT 01-NOV-1997 (Rel. 35, Created)
4	4885	66.8	1403	1	BIRF_MOUSE	DT 16-OCT-2001 (Rel. 40, Last sequence update)
5	4811	65.8	1402	1	BIRG_MOUSE	DT 01-MAR-2002 (Rel. 41, Last annotation update)
6	4796.5	65.6	1024	1	CARC_HUMAN	DE Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis inhibitory Protein).
7	654	8.9	1024	1	BIR3_HUMAN	DE BIRC1 OR NAIP.
8	462	6.3	618	1	BIR4_RAT	GN Homo sapiens (Human).
9	457.5	6.3	612	1	BIR3_MOUSE	OS BIR4_MOUSE; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
10	440	6.0	600	1	BIR2_MOUSE	OC
11	436.5	6.0	604	1	BIR2_HUMAN	NCBI_TaxID=9606;
12	431.5	5.9	496	1	BIR4_MOUSE	[1] RP SEQUENCE FROM N.A.
13	416.5	5.7	496	1	BIR4_RAT	RC TISSUE=Brain;
14	407	5.6	497	1	BIR4_HUMAN	RC MEDLINE=9311234; PubMed=7813013;
15	388	5.3	611	1	BIR4_CHICK	RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Yaraghi Z.,
16	335	4.6	498	1	IAP2_DROME	RA Salin M., Aubry H., Tamai K., Guan X., Ioannou P., Crawford T.O.,
17	326	4.5	358	1	PIAP_PIG	RA de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.;
18	303.5	4.2	275	1	IAP_GYCP	RT "The gene for neuronal apoptosis inhibitory protein is partially deleted in individuals with spinal muscular atrophy.";
19	301	4.1	438	1	IAP1_DROME	RT deleted in individuals with spinal muscular atrophy.";
20	293.5	4.0	268	1	IAP3_NEVOP	RT Cell 80:167-178(1995). [2]
21	201.5	2.8	1062	1	NALL_HUMAN	RP SEQUENCE FROM N.A., AND REVISIONS.
22	198	2.7	1473	1	NALL_HUMAN	RT Sequence of a 131-kb region of S913.1 containing the spinal muscular atrophy candidate genes SMN and NAIP.";
23	194.5	2.7	997	1	BIRL_SCHPO	RT Genomics 48:121-127(1998). [3]
24	192	2.6	1453	1	VP15_YEAST	RP SEQUENCE OF 386-623 FROM N.A.
25	182	2.5	953	1	CAR4_HUMAN	RA der Stege G., Draaijers T.G., Grootenhuis P.M., Osinga J.,
26	180.5	2.5	3210	1	CENP_HUMAN	RA Anzivino R., Velona L., Brahe C., Scheffer H., van Ommen G.J.B.,
27	175.5	2.4	275	1	IAP1_NEVOP	RA Subs C.H.C.M., Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
28	167	2.3	4540	1	DYHC_PARTE	RR Jones K., Graves T., McPherson J.;
29	166.5	2.3	1040	1	CARF_HUMAN	RR Jones K., Graves T., McPherson J.;
30	165.5	2.3	1315	1	CHAO_DROME	RR Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
31	164.5	2.3	286	1	IAP1_NEVAC	RR [5] FUNCTION.
32	163	2.2	239	1	ZFP_IRV6	RC TISSUE=Liver;
33	162	2.2	1041	1	TLR8_HUMAN	RC MEDLINE=93149219; PubMed=8552191;
						RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
						RA Parhami R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.,
						RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes";
						RL Nature 370:349-353(1996).
						CC -1 FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF SIGNALS.

CC - TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY  
 CC NEURONS, FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN  
 CC SPINAL CORD.

CC - DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN  
 CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMI TYPE I). SMAS  
 CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I  
 CC (WERDING-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE  
 CC III (MOHLFART-KUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF  
 CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE  
 CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO  
 CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERN IS 1 IN 600  
 CC NEWBORNS.

CC - SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC - SIMILARITY: CONTAINS 1 NACHT DOMAIN.

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DR EMBL: U19351; AAC52045.; -  
 DR EMBL: U80017; AAC52047.; -  
 DR EMBL: U21913; AA64504.; -  
 DR EMBL: AC005031; AAC62261.; -  
 DR HSSP: Q1490; 1QBH.  
 DR MM: 600355; -  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR; 3.  
 DR SMART: SM0236; BIR; 3.  
 DR PROSITE: PS0128; BIR\_REPEAT\_1; 3.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 KW Apoptosis; Repeat; REPEAT; REPEAT; REPEAT; REPEAT; REPEAT; REPEAT;  
 FT REPEAT 159 227 BIR 1.  
 FT REPEAT 278 345 BIR 2.  
 FT DOMAIN 464 758 BIR 3.  
 FT CONFLICT 222 223 NACHT.  
 FT CONFLICT 386 387 PRK -> YR (IN REF. 4).  
 FT CONFLICT 535 535 VP -> ST (IN REF. 3).  
 FT CONFLICT 553 553 M -> V (IN REF. 3).  
 FT CONFLICT 1228 1231 Y -> H (IN REF. 3).  
 FT SEQUENCE 1403 AA; 159613 MW; 566304C154DA564 CRC64;

Query Match 100.0% Score 7308; DB 1; Length 1403;  
 Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATQOKASDERISQFDHNLPELSALLGLDVAQVLAKELEEEQQERAKMOKGYNQSMSE 60  
 1 MATQOKASDERISQFDHNLPELSALLGLDVAQVLAKELEEEQQERAKMOKGYNQSMSE 60  
 QY 61 AKRLKTFVYEPSSWMPQEMAAGPFPTGKSGTCFCSSLIFGAGITRPLIEDKRF 120  
 61 AKRLKTFVYEPSSWMPQEMAAGPFPTGKSGTCFCSSLIFGAGITRPLIEDKRF 120  
 Db 121 HPGCGFLINKDVGNTAKYDIRVKNIKSRURGGKRYOEEEARLASFRMWPFLVQGISPCV 180  
 Db 121 HPGCGFLINKDVGNTAKYDIRVKNIKSRURGGKRYOEEEARLASFRMWPFLVQGISPCV 180  
 QY 181 LSEAGEFVFTGQDVTQFCSCGGCLGNWEGDPPKEHAKWPKCEFLRSKKSSEITQYI 240  
 181 LSEAGEFVFTGQDVTQFCSCGGCLGNWEGDPPKEHAKWPKCEFLRSKKSSEITQYI 240  
 QY 241 OSYKGFVDITGEHFTVNSWTOREJUMASYCNISIATEELRSDKWDPRSAVVAALA 300  
 241 OSYKGFVDITGEHFTVNSWTOREJUMASYCNISIATEELRSDKWDPRSAVVAALA 300  
 QY 301 KAGFYFTGKRDIVOCFSGGGCLEKWMQEGDDPLDDH'RCFPNCPLQNMKSSAETPDQS 360  
 301 KAGFYFTGKRDIVOCFSGGGCLEKWMQEGDDPLDDH'RCFPNCPLQNMKSSAETPDQS 360

Db 301 KAGLYFGIKIVQCPSCGSCLEKWMQEGDDPLDDH'RCFPNCPLQNMKSSAETPDQS 360  
 QY 361 RGCCLCELETTSSESNLDSIAVGPVPIVEMAOGENAQWQEQAEKNEOLRAATSAEPRHMS 420  
 361 RGCCLCELETTSSESNLDSIAVGPVPIVEMAOGENAQWQEQAEKNEOLRAATSAEPRHMS 420  
 Db 421 LDITSSDLADHLLGCDLSIASKHTSKWQEPVLPEVGNLSVMCVCBEGSCKTL 480  
 421 LDITSSDLADHLLGCDLSIASKHTSKWQEPVLPEVGNLSVMCVCBEGSCKTL 480  
 Db 481 KKIAFLWASGCCPLNRPOLVFYLSSTRPDEGLASICODOLLKREGSTTEMORNITQ 540  
 481 KKIAFLWASGCCPLNRPOLVFYLSSTRPDEGLASICODOLLKREGSTTEMORNITQ 540  
 QY 541 OLKNQVNLFLDDYKEICSIPOVIGKLIQKNIHLRSCTLLIAVTRHARDYRMLTLEIK 600  
 541 OLKNQVNLFLDDYKEICSIPOVIGKLIQKNIHLRSCTLLIAVTRHARDYRMLTLEIK 600  
 QY 601 AFPYNTVCLRKLFESHNMTRKENVFKKNQSLQKLTQTPLEVAATCAHPOYPPS 660  
 601 AFPYNTVCLRKLFESHNMTRKENVFKKNQSLQKLTQTPLEVAATCAHPOYPPS 660  
 Db 661 FDDVAVKSYMERLSLRNKATAEIKATVSSCGELALKGFSCCFEFNDDDLAEAGVED 720  
 661 FDDVAVKSYMERLSLRNKATAEIKATVSSCGELALKGFSCCFEFNDDDLAEAGVED 720  
 QY 721 EDLTMCMLSFTAQSLRPPYRFLSPAFOEFLAGMRLLSDRQEIQDGLYHJKQNS 780  
 721 EDLTMCMLSFTAQSLRPPYRFLSPAFOEFLAGMRLLSDRQEIQDGLYHJKQNS 780  
 Db 781 PMMTVSAYNNFLNVSSLSPKSTKAGPKTVSHLHVNDKESLENISENDYKLHOPEISQ 840  
 781 PMMTVSAYNNFLNVSSLSPKSTKAGPKTVSHLHVNDKESLENISENDYKLHOPEISQ 840  
 QY 841 MOLRGQLNQICPAQFYSVSHLHVALKTAVOSNTIVACSPFLQFLQCRRTLGAQNL 900  
 841 MOLRGQLNQICPAQFYSVSHLHVALKTAVOSNTIVACSPFLQFLQCRRTLGAQNL 900  
 Db 901 QYFDPHPSLSLRSIHPGRNKTSPRAHSVFLCFSKDKSQVNPIDQYASAPPMNEW 960  
 901 QYFDPHPSLSLRSIHPGRNKTSPRAHSVFLCFSKDKSQVNPIDQYASAPPMNEW 960  
 Db 961 ERNLAEKEDNYKSYMMDORMRASPDLSTGYWKLSPKQYKIPCLIEVDVNDIVGQDMILEI 1020  
 961 ERNLAEKEDNYKSYMMDORMRASPDLSTGYWKLSPKQYKIPCLIEVDVNDIVGQDMILEI 1020  
 Db 1021 MIVFASASORLILHNHSRGTESIRPALILSKASVTKCISKIELSAAEQLLTLPSL 1080  
 1021 MIVFASASORLILHNHSRGTESIRPALILSKASVTKCISKIELSAAEQLLTLPSL 1080  
 Db 1081 SLEVSGTQSQQDFPNUKDFLKFLKELSVLDGNNINFSVPEEFNPHMEKLIQISA 1140  
 1081 SLEVSGTQSQQDFPNUKDFLKFLKELSVLDGNNINFSVPEEFNPHMEKLIQISA 1140  
 QY 1141 EYDPSKLVKLIQNSPNLPHAKCNFESDFGSLMTMVSKKLTTEKFSDSFQAVPFA 1200  
 1141 EYDPSKLVKLIQNSPNLPHAKCNFESDFGSLMTMVSKKLTTEKFSDSFQAVPFA 1200  
 Db 1201 SLPPFISKILNLQGQPDDETERSEFAYIIGLSSLNLEELIJLPTGDIYVRAKLIQOCA 1250  
 1201 SLPPFISKILNLQGQPDDETERSEFAYIIGLSSLNLEELIJLPTGDIYVRAKLIQOCA 1250  
 Db 1251 PNLQDLSRTEICKAQATTVKSLSCVLRPLRILNMLSWLADDATLANTMKER 1380  
 1251 PNLQDLSRTEICKAQATTVKSLSCVLRPLRILNMLSWLADDATLANTMKER 1380  
 QY 1321 PNLQDLSRTEICKAQATTVKSLSCVLRPLRILNMLSWLADDATLANTMKER 1380  
 1321 PNLQDLSRTEICKAQATTVKSLSCVLRPLRILNMLSWLADDATLANTMKER 1380  
 QY 1381 HQSKLTILQKWLPPSPIQ 1403

Db	1381 HPQSKYLTILQKWLUPFSPIQK 1403	FT	CONFLICT	1269	1269	A -> V (IN REF. 3).																																																																									
SQ	SEQUENCE	1403 AA;	158692 MW;	B3163025955EE67	CRC64;																																																																										
RESULT	2																																																																														
BIR_A MOUSE	STANDARD:	PRT:	1403 AA.																																																																												
ID	BIR_A MOUSE	ID	Q9WKS5; Q9R017; Q9TB5;																																																																												
AC		DT	16-OCT-2001 (Rel. 40, Created)																																																																												
DT		DT	16-OCT-2001 (Rel. 40, Last sequence update)																																																																												
DT		DT	01-MAR-2002 (Rel. 41, Last annotation update)																																																																												
DE		DE	Baculoviral IAP repeat-containing protein 1a (Neuronal apoptosis inhibitor protein 1).																																																																												
GN		DE	BIRCIA OR NAIP1 OR NAIP.																																																																												
OS		MUS musculus (Mouse)																																																																													
OC		Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.																																																																													
NCBI_TAXID	10090;	RN	[1]																																																																												
RP	SEQUENCE FROM N.A.	RN																																																																													
RX	Yarachli Z., Korneluk R.G., Mackenzie A.E.; MEDLINE=95431676; Pubmed=10501978;	RX																																																																													
RA	"Cloning and characterization of the multiple copies of the murine homologue of Naip (neuronal apoptosis inhibitory protein).";	RA																																																																													
RT	"The mouse Naip gene cluster on Chromosome 13 encodes several distinct functional transcripts.";	RT																																																																													
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.	RL	[2]																																																																												
RN		RN																																																																													
RP	SEQUENCE FROM N.A.	RP																																																																													
RX	Medline=20414747; Pubmed=10958627;	RX																																																																													
RA	Huang S., Schaff J.M., Grawney J.D., Endrizzi M.G., Dietrich W.F.;	RA																																																																													
RT	"Genomic sequence analysis of the mouse Naip gene array.";	RT																																																																													
RL	Genome Res. 10:1095-1102(2000).	RL																																																																													
CC	-1- FUNCTION: PREVENTS MOTOR NEURON APOPTOSIS INDUCED BY A VARIETY OF SIGNALS.	CC																																																																													
CC	-1- SIMILARITY: CONTAINS 3 BIR REPEATS.	CC																																																																													
CC	-1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.	CC																																																																													
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	CC																																																																													
CC	EMBL; AF007769; AABG9223; 1. DR EMBL; AF135491; AAD56763; 1; DR EMBL; AF242432; AAF82752; 1; DR HSSP; Q13490; IQBIR; DR MGD; MGII:1298223; Bircia; DR InterPro; IPR001370; BIR; PRAM; PF00653; BIR; 3. DR SMART; SM00238; BIR; 3. PROSITE; PS01282; BIR_REPEAT_1; 1. PROSITE; PS50143; BIR_REPEAT_2; 3. PROSITE; PS50837; NACHT; 1. KW APPOSIS; Repeat; Multigene family. FT REPEAT 60 127 BIR 1. FT REPEAT 159 227 BIR 2. FT REPEAT 278 345 BIR 3. FT DOMAIN 464 758 NACHT. FT CONFLICT 343 343 I -> V (IN REF. 2); L -> O (IN REF. 2); E -> K (IN REF. 2); D -> N (IN REF. 3); D -> N (IN REF. 3); G -> R (IN REF. 1); L -> H (IN REF. 1); T -> M (IN REF. 2).	FT	CONFICT	1269	1269	A -> V (IN REF. 3).																																																																									
Query	Match	Match	67.8%	Score	4956	DB 1; Length 1403; Best Local Similarity 58.4%; Pred. No. 2, 7e-285; Indels 0; Gaps 0; Matches 958; Conservative 158; Mismatches 285;																																																																									
Matches	958;	Matches																																																																													
OY	1	MATQQKASDRIQSOPDHNLPELSALLGLDAVOLAKELFEEQERAKAOQKGNSQMRSE 60	OY	1	MAEHGESSESDRIDESEIDYFLPELSALLGVDVOLAKSOFEFEHFERMKLKKGNSMRSE 60	OY	61 AKRLKTFVTTPEPYSSWIPQEMAAGFYFTGVSGTQCFCSLILFGAGITRLPTEDHKKF 120	OY	61 AKRLKTFETTDFTFREWTQPMAGFYHTQVKLGWCRCSSLIFGNNSRKLPIERHKL 120	OY	121 HPDCCFLLNKDVGNIAKYDVKNUKSRKRGKMYOERBARLASFRNNPPYVGISPV 180	OY	121 RPECBFLOGKVGVGNIGKDYRVSKEPKMLRGKARYHECARLESFEDPPFYAHGTSPRV 180	OY	241 OSYKGFVDTGEHFNWSWORELPMASACNDNSFAYEIRLDSFKDWAPRESAVGAALA 300	OY	241 LSEAFVFVGKQOPTVQCSGGCLGNWECDPKEHAKWFPKCEFLRSKKSSEITQI 240	OY	181 LSAAGFVFITSKRDVTQFCSCGGSLGNWECDPWPKEHAKWFPKCEFLRSKKSSEITQI 240	OY	301 KAGLFYTGKIDIVOCFSCGGCLEKNOEGDDPLDHTTRCPNCPCFLQNMSSAEPDQLS 360	OY	301 RAGLFYTGKIGIVODFSCGGMEKTEGDDPPIOEHNKFNPNCIFLQTPTQSSAEVIPALL 360	OY	421 LUDISSDLATDHLGCGDLISLASKHISKQPKOEPVPLPEVFGNLSVACVCEAGSCKTLL 480	OY	361 RGEGLFELLETTSESNELEDSTAVGPIVPEMAQGAQWFOAKNLMQEQLRAYTSFRHS 420	OY	361 HCAALPEAMETTSSENHDDPAVHSTVGLGRSEAOWFQEARSLSBOLRNUYKATFRHM 420	OY	481 KRIAFWASGCCPLNRFQVYISLSSTRDEGLASICIDQOLKEKEGSTTEMCRNII 540	OY	481 KRIAFWASGCCPLNRFQVYISLSSTRDEGLASICIDQOLKEKEGSTTEMCRNII 540	OY	481 KRIAFWASGCCPLNRFQVYISLSSTRDEGLASICIDQOLKEKEGSTTEMCRNII 540	OY	541 OLKNOLFUDYKEDKECISPIVQIGLIQKHLRSRCLLAVTRHARDIRRYLEILEK 600	OY	541 OLKNOLFUDYKEDKECISPIVQIGLIQKHLRSRCLLAVTRHARDIRRYLEILEK 600	OY	541 OLQHQVFLFLUDYDGSGLSPOALHTLITKVNLSRCLLAHVTHNRVGRJRSYLDLSIEK 600	OY	601 AFPNTIVTCIRKLFHNTRKMYVQKNSQKIOKTPLEVARICAHWFQYPFDSS 660	OY	601 AFPNTIVTCIRKLFHNTRKMYVQKNSQKIOKTPLEVARICAHWFQYPFDSS 660	OY	601 EFPLSNTYIKLFFSHNIRKLEMPVNGYGENEDLQGKTLPEAVTDWFENPSDQ 660	OY	661 FDDAVVKSYMERLSLRNKATAEILKATVSSCGELALKGRFSCCFEFNDDLAEGVDD 720	OY	661 FDDAVVKSYMERLSLRNKATAEILKATVSSCGELALKGRFSCCFEFNDDLAEGVDD 720	OY	661 FQDMALFKSTMQYLSKHKGAQPLQTSQCGQJALTGFSSCREFNSDLDABGVDED 720	OY	721 EDUTMCLMSKETAORLPRFPLFSAFOEPLAGMLIELSDPQEHQDGLYHUKOINS 780	OY	721 EDUTMCLMSKETAORLPRFPLFSAFOEPLAGMLIELSDPQEHQDGLYHUKOINS 780	OY	781 PMMTVSAYNVLNYVSSLPSKTAGRKIVSHLHLVDNKSENLENSENDYKLHOPEISQ 840	OY	781 PMMTVSAYNVLNYVSSLPSKTAGRKIVSHLHLVDNKSENLENSENDYKLHOPEISQ 840	OY	781 PLKAUTTYNNFLKPVSHSSKAGTVPHVSHLHLVDTELLENTYKNEYVNHPGTSRI 840	OY	841 MQLRGLWQICPOAVFSMVSBEHLLVALKTAYOSNTVAACSPFVIQFLQGRTLTGALN 900	OY	841 MQLRGLWQICPOAVFSMVSBEHLLVALKTAYOSNTVAACSPFVIQFLQGRTLTGALN 900	OY	841 MKGLKELWLLSPEYSSFVSEHLLKALNAYESTVACASPFVIQFLQGRTLTGALN 900	OY	901 QYFFHPEISLRLSRIHFTRGKNSPRAFHSVLTFCFSQVTFIDYDASYAREPMNW 960	OY	901 QYFFHPEISLRLSRIHFTRGKNSPRAFHSVLTFCFSQVTFIDYDASYAREPMNW 960	OY	901 QYFRDHPESLULVKSLEVSVINGKPVVWDYDSVMEKSFETLQPPMTDQYDASYAEQMKER 960	OY	961 ERNLAEKEDNVKSYMDMQRASPDLSTGVWKLSPQYKTPCLEVDVNDIDVVGQDMLET 1020	OY	961 ERNLAEKEDNVKSYMDMQRASPDLSTGVWKLSPQYKTPCLEVDVNDIDVVGQDMLET 1020

Db	961 EKNLSENEETIKTSKINFPPLQPKISSGYWKLSPRKCKPFRLEVGUTNGPAQDQLQV	R.A	Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
Qy	1021 MTVESASQRRIELHNRGFIIRSPALELSKASTYKCSITSKELSAEQEULLTSPLE 1080	R.A	Kunzel L.M., Dietrich W.F.,
Db	1021 MEFASASOIEFLRSOSFESTIRALELSKASVTRKUSMSRLSRAEOLLTUPLQ 1080	R.T	"The mouse region syntonic for human spinal muscular atrophy lies within the Lgnl critical interval and contains multiple copies of Naip exon 5." -
Qy	1081 SLEVSQGTQSQQIFNLUFLCLUEKLSVDEGENINVSVIPEEPFHMEKLLTQISA 1140	R.L	Genomics 38:405-417(1995).
Db	1081 SLEVSETNQLPDOLFLNHFLRKGFLGUKELCVRLDQKPDVLVSLVQGEFFNLHNEKLSIRT 1140	C.C	-I- SIGNALS.
Qy	1141 ETDPSKLUKLIQNSNLHFLHKNCNFSDGSIMTMVLSCKERKPFSSQFQAVPFA 1140	C.C	-I- SIMILARITY: CONTAINS 3 BIR REPEATS.
Db	1141 ESDLSKLVKLQIIONSPNLHVFLKCDFLSNCDLAVIASCKLRETEFSGRCFEMAPFV 1200	C.C	...-----
Qy	1201 SPNPNTISKILNLLEGQQPDEETSEKFAYIGLSLSNLEELLPLPDGIVRALKLITCQ 1260	C.C	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
Db	1201 ILPNFISKLNLISQGPDKETSEKFAQALGSLRNLEELVPIPGGHQVAKLIVROL 1260	C.C	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> ).
Qy	1261 OLBOLURVLSFKTLNLDDSWVLAKVAGSGQKLENKLISINHKITERGYSRFOALDN 1320	C.C	...-----
Db	1261 OLPCURVLAHYLDNSVILARVATSGGFQKLEKLDLSMHKITEGYRNFQALDN 1320	C.C	...-----
Qy	1321 PNLQNLNCTCRHIPECTIQVQATVTVKALGCVSRPLSLTRLHMLSWLLODEEDAKVINDVER 1380	D.R	DR EMBL; AP135490; AAD56761; -.
Db	1321 PNLQNLNCTCRHIPECTIQVQATVTVKALGCVSRPLSLTRLHMLSWLLODEEDAKVINDVER 1380	D.R	DR EMBL; AP13205; AAD56759; -.
Qy	1381 HPOSKYLTILQKWLWPSPPI 1401	D.R	DR EMBL; U66329; AAC52977; -.
Db	1381 HPOSKYLTILQKWLWPSPPI 1401	D.R	DR HSPB; Q13490; IQBH.
Qy	1401 HPOSKYLTILQKWLWPSPPI 1401	D.R	MGI; MGI:1298246; Bircbl.
RESULT	3	D.R	InterPro: IPR01370; BIR.
BIRB_MOUSE		D.R	PFam: PF00653; BIR; 3.
ID		D.R	SMART: SW00238; BIR; 3.
BIRB_MOUSE		D.R	PROSITE: PS01182; BIR_REPEAT_1; 2.
AC	Q9Q444; Q9R030; O09124;	D.R	PROSITE: PS50143; BIR_REPEAT_2; 3.
DT	16-OCT-2001 (Rel. 40, Created)	K.W	NACHT; 1.
DT	16-OCT-2001 (Rel. 40, Last sequence update)	F.T	Apoaposis; Repeat; Multigene family.
DE	01-MAR-2002 (Rel. 41, Last annotation update)	F.T	REPEAT
DE	Baculoviral IAP repeat-containing protein 1b (Neuronal apoptosis inhibitory protein 2).	F.T	159 227
DE	BIRC1B OR NAIP-RS6.	F.T	BIR 1.
OS	Mus musculus (Mouse).	F.T	REPEAT
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Oxfam; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	F.T	508 802
RN	[1]	F.T	BIR 3.
SEQUENCE FROM N.A.		F.T	DOMAIN
RX	MEDLINE 9831676; PubMed=10501978;	F.T	377 345
RX	Huang S., Scharf J.M., Gromley J.D., Andrizzi M.G., Dietrich W.F.; The mouse Naip gene cluster on Chromosome 13 encodes several distinct functional transcripts.;	F.T	NACHT.
RX	Mamm. Genome 10:1032-1035(1999).	F.T	403 478
RF	SEQUENCE FROM N.A.	F.T	CONFFLICT
RF	MEDLINE=991542; PubMed=10384056;	F.T	478 540
RA	Yarchoh Z., Diez P., MacKenzie A.; cDNA cloning and the 5' genomic organization of Naip2, a candidate gene for murine leg ionotrola resistance.;	F.T	CONFFLICT
RL	Mamm. Genome 10:761-763(1999).	F.T	862 1079
RC	SEQUENCE FROM N.A.	F.T	CONFFLICT
RC	STRAIN=29/SV;	F.T	1079 1080
RY	MEDLINE=991574; PubMed=10466205;	F.T	SD -> FN (IN REF. 3).
RA	Kunkel L.M., Miller W., Dietrich W.F.; Comparative sequence analysis of the mouse and human Lgn1/SMA Genomics 60:137-151(1999).	F.T	1089 1091
RA	Strain=29/SV;	F.T	R -> C (IN REF. 3).
RA	Strain=29/SV;	F.T	1115 1115
RA	Strain=29/SV;	F.T	K -> E (IN REF. 3).
RA	Strain=29/SV;	F.T	T -> A (IN REF. 3).
RA	Strain=29/SV;	F.T	1122 1126
RA	Strain=29/SV;	F.T	1136 1136
RA	Strain=29/SV;	F.T	D -> E (IN REF. 3).
RA	Strain=29/SV;	F.T	1157 1157
RA	Strain=29/SV;	F.T	S -> G (IN REF. 3).
RA	Strain=29/SV;	F.T	1167 1167
RA	Strain=29/SV;	F.T	G -> R (IN REF. 3).
RA	Strain=29/SV;	F.T	1271 1271
RA	Strain=29/SV;	F.T	F -> C (IN REF. 3).
RA	Strain=29/SV;	F.T	SEQUENCE
RA	Strain=29/SV;	F.T	1447 AA; 164033 MW; 9EE6C6A73BAE60A2 CRC64;
Query Match	Best Local Similarity	Matches	67.3%
	Score	4919;	DB 1;
	Pred.	No.	4.4e-284;
	Conservative		
	Mismatches		Length 1447;
	Indels		
	Gaps		
Qy	1 MATQOKASDERISOFDHNLPELSLGLIDAVQAKLEEEERAKMQKGNNSMRSE 60	D.b	1 MAQAGEAVEEICEFDDDLVSELSTLRLYDALSVLRKQOEEDHTRMKKGPNQMRSE 60
Qy	61 ARKLKTFVTPYSSWPMAGFTGVMGSIQFCCLSILFGAGLTRLRPEDHKRP 120	D.b	61 AKRLKTFPTEIDFRSWTPOEMAAGFYHTGVKGVOCCSCLLFLSTRLRKLPENHKKL 120
Qy	121 HDCCGPILLNDVGNIAKYDIRVNLKSLRGGMRMYYQEEARLASFRRMPYVQGICV 180	D.b	121 RPPCEFLICKDVGNGKDYIRVSPERMRLDKARYTHEEARLSSPEDWPFYAHGSPV 180
Qy	181 LSEAGFVFVQKOTVQFSCGGCLGWNNEGDPPWHEAHWKPKCEPLRSKSESEIYOI 240	D.b	181 LSAAGFVFVQKRTDVOCFSCGGCLGWNWEEDDPWHEAHWKPKCEPLRSKSESEIYOI 240





RP  
SEQUENCE OF 82-168 FROM N.A.  
RC STRAIN=128/SVJ;  
MEDLINE=97131520; PubMed=8975718;  
RA Scharf J.M., Damon D., Frisella A., Bruno S., Beggs A.H.,  
RA Kunkel L.M., Dietrich W.F.;  
RT "the mouse region syntetic for human spinal muscular atrophy lies  
within the LgN1 critical interval and contains multiple copies of Naip  
exon 5.";  
RL Genomics 38:405-417(1996).  
CC -!- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.  
CC -!- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC  
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CC  
EMBL; AF42431; AAB8275\_1; -.  
DR EMBL; U65327; AAC52975\_1; -.  
DR MGD; MGII-129822; Birclf.  
DR InterPro; IPR01370; BIR.  
DR Pfam; PF00653; Bir; 3.  
DR SMART; SM00238; Bir; 3.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE; PS50337; NACHT; 1.  
KW Apoptosis; Repeat; Multigene family.  
FT Repeat 60 127 BIR 1.  
FT Repeat 159 227 BIR 2.  
FT Repeat 278 345 BIR 3.  
FT DOMAIN 464 759 NACHT.  
SEQUENCE 1403 AA; 159823 MW; 9d4912503358c4e9 CRC64;

Query Match 65.8%; Score 4811; DB 1; Length 1403;  
Best Local Similarity 66.3%; Pred. No. 1.1e-27;  
Matches 929; Conservative 174; Mismatches 297; Indels 2; Gaps 2;

QY 1 MATQQKASDERIQSQFDHNLPELSALLGLDAVLAKEEEERAKERAKMKGQNSQMRSE 60  
|| ::||| :||| :| |||| |::||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| |||

Db 421 LPEVSSLGTDHLUGCDVSITSKHYSQPVGALTIPEFVNLSVCGEAGSGKTF 480  
Oy 481 KKIELWASSGCCPLUNRQFLVFLSLSSTRPDEGLASIDOLIJKEGSYEMRNIIQ 540  
Db 481 KRIAFLWASSGCCPLUYRFLQVFLSLSSTRDQGANLICITQDLYLAGGCSEVCLSSIQ 540  
Qy 541 QLKNOVLFLLDDYKEYCSTPOVIGKLIQKHLRSRTLCLAVTRNARDYRYLETEIK 600  
Db 541 OLHQYLFLLDDYSLGSQALHLPLTQLYFLRCFLLAIVHNRVDRPYTSLEIQ 600  
Qy 601 AFPYNTVCILRKPSHMTRKMFVYRCKNQSKQIKTQPLFVAIAAHWFQ-YPEP 659  
Db 601 BPFINTVFLRKFFSHDIICEVKELIYSENKDQGVYKIPFLVAEVNDWNQNAQD 660  
Qy 660 SFDDYAVKSYMERLSLRNATAELTKAVTSSCGELAGLGFSCFEPFDLLEAGVDE 719  
Db 661 DFQDVTLFHSMYQMSLKLKYKATAESLQATVSSCGOLALNTLFLSSCFEFNSDDEAAGVDE 720  
Qy 720 DEDLTMCMSKFTQRRLPYTRELSPAFQDFLAGMLIEELDSRQEQHDGLYHLQIN 779  
Db 721 DVKLTTPLMSKFTAGRLPVYRGLPQDFLAFLVLLSPDQDGLYLYLROD 780  
Qy 780 SPMMTWSAYNNFLNVSSFLSTKAGPKIVSFLHVDNLESLENSENDYDLKHQPEISL 839  
Db 781 SPLKLNFSNFNLFYVSSHSKAAPTVSHLQDLYDERESLENNSENDYDMKUHQPTL 840  
Qy 840 OMQLRGUMQICPOQYFMSYEHLLVLAKTAYNTVACSPVLTQFLQFGRQLTJGALN 899  
Db 901 LEYFNHDPESSILLRSKUSLRSKUSLRSKUSLRSKUSLRSKUSLRSKUSLRSKUSLRS 900  
Qy 960 WERNLAEKDNVSKYMDMORASPDLS37WKLSPROYKIPCLEVNDVNDVQADMLT 1019  
Db 960 WRRNFAQDEPIKNEYNTWALPDISE37WNLSPKPCIPKLEVNQNNPAGDQALQV 1019  
Qy 1020 LMVTFVSASORIELHLNSRFIESIRPALELSKASYTKSISKELSAAEQLLTPLS 1079  
Db 1020 LMEVFSASQSIEFHFLNFSGFLESIRPALELSKASYTKSISKELSAAEQLLTPL 1079  
Qy 1080 ESLEYSGTQSQDOPFLNPDKFLCKELSYDLEGINSVNPYFVHFKCONFPDSLMTMLYSLCKKLTIEKSDSFQAVPV 1199  
Db 1080 QSLEVSETNOLPDOLHNLHKFLGKLGKFLCVRDGPVLSPEFLNHLHMEKLRS 1139  
Qy 1140 AEYDPSLKVLIQNSPNLHVFLKONFPDSLMTMLYSLCKKLTIEKSDSFQAVPV 1199  
Db 1140 TESDLSKLVFIQNPFLHVFLKODFLSNCESINTALSKKREIESQOCQTEAMFV 1199  
Qy 1200 ASLPNPISKLINLREGQQFDEETSEKFAYTGSLSNLBRBLILPQDGTYRVALIIOQC 1259  
Db 1200 NILPFPVSLKLSKGQFADKETSEKFPAOLGLSRNLNELLVFTGDIHOVAKLIVRC 1259  
Qy 1260 OQRCGLRVISFFKTUNDSTVEIAKVAIGGFOKLENLKSINKITEGSYRNFOALDN 1319  
Db 1260 LQLPCLRVIAFHDLUDDEVEIGAEATGCSFQKLNLDJSMHRTKITEGCRNFOALDN 1319  
Qy 1320 MPNQELDISRHFTECAQTWKLSCVLRLPRLRILNMSWLADDIALNVMKE 1379  
Db 1320 LPNQLMNLCRNIGRIQVATTVKALGHCVSRUPSLTRIGMLSWLADDIDALNVMKE 1379  
Qy 1380 RHPQSKYLTQKWLPEPSIT 1401  
Db 1380 RHPQSKRLLFWKMLVPEPSPV 1401  
RESULT 6  
BIRG\_MOUSE ID BIRG\_MOUSE STANDARD PRT 1402 AA.  
AC 09JFB3; DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis  
 DE Inhibitory Protein 7).  
 GN BIRCIG OR NAIP7.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI-TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20414747; PubMed=10958627;  
 RA Endrizzi M.G., Hadinoto V., Groomey J.D., Miller W., Dietrich W.F.;  
 "Genomic sequence analysis of the mouse Naip gene array.",  
 Genome Res. 10:1095-1102(2000);  
 -1. FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
 CC SIGNALS.  
 -1. SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1. SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
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 CC EMBL; AF242433; AF82791; -  
 DR MGI-1858256; Bircig.  
 DR InterPro; IPR001370; BIR.  
 DR Pfam; PF00653; BIR; 3.  
 DR SMART; SM00228; BIR; 3.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
 KW Apoptosis; Repeat; Multigene family.  
 FT REPEAT 60 127  
 FT REPEAT 159 227 BIR 1.  
 FT REPEAT 278 345 BIR 2.  
 DOMAIN 454 759 BIR 3.  
 SEQUENCE 1402 AA: 159662 MW: CIDFFBA359893ECD CRC64:  
 Query Match 65.6%; Score 4796.5; DB 1; Length 1402;  
 Matches 931; Conservative 171; Mismatches 297; Index 3; Gaps 3;  
 Qy 1 MATQOKASPERISOFDHNLLEPSALGLDAVOLAKELERBEBOKERAKOMQKGYNQNSMRSE 60  
 Db 1 MAHEGESSERDRISBIDEFLANLSAREGNGMNLQVQLKSQEDDHMERMKKGNSMRSE 60  
 Qy 61 AKRKKTFVYEPYSSWFOEMAAGYFTGVKSGQFCFCSLLIFGAGLTRLTIEDIKRF 120  
 Db 61 AKRKLTKTFESYDPRFSWMPQEMAAAGFYHTGVKSLQFCFCSLLIFGNSLRKPLIERKKL 120  
 Qy 121 HPGCGFLINKLVNQIARYDIKVKNKSRLRGKARYQEEARLASFRNPWPFYQGSPCV 180  
 Db 121 RPECEFLQGKQVNGKYDTRVKSPERMKRGKARYHEEARLESFDWPPYAHGSPRV 180  
 Qy 181 LSEAGVFTGKQDTCQCFSGCGCQMGEGDPWPKHEAKWPKCERLKSKSESTOYI 240  
 Db 181 LSAAGEVFTGKQDTCQCFSGCGSGLGNWEGDDPKEHAKWPKCERLKSKSESTOYI 240  
 Qy 241 OSYKGVUDTGEHFNSWQRELFMASYCNDFAYEELRDSFKWPRESAVVAALA 300  
 Db 241 OGYEGFVHVHGHEVHKSWWRLEPMVSAYCNDSVFANEELMDMWDQESPGVVEALV 300  
 Qy 301 KAGGFYTGKQDTCQCFSGCGCERLKWKQEGDPPLADDITRCFPCNPCLPQFQNMSSAETPDQS 360  
 Db 301 RAGFYTGKQDTCQCFSGCGCERLKWKQEGDPPLADDITRCFPCNPCLPQFQNMSSAETPDQS 360  
 Qy 361 RGECELLETTSENLDSDINGPPIPPEMAOGAEAMQFOEAKNLJEFQRLRAYTASFRMS 420

Db 361 QYLPEATETTRESNHGDAAVHSTVDIGRSEAOFWOBARSUSEQRDTVTKTSFCHMN 420  
 Qy 421 LI DISSDATPHLGDLS T ASKHSK P Q EPLVPEVFQGNLNSVM C VEGAGSGTIVL 480  
 Db 421 UPEVCSSLGDHLS C DVS LISKHSQ P Q V GALT P E V F S M S V M C V E G A G S K T V L 480  
 Qy 481 KKIAFWAASSGCCPLNRFQFLVFLSSTRPDEGLASITCDOOLEKGSTEMCRNIT 540  
 Db 481 KRIATLWASSCCPPLYREFQFLVFLSSTTPQGDMLICQDMLCQLGAGCISEVCLSSIQ 540  
 Qy 541 QLKNOVFLPFLDDYKEICSPQVIGLQKHNLSRTCLIAVRTNRARDIRYLETILEK 600  
 Db 541 QLQHOVLELDYDGSGLSPQALHNTKLYTCLLAVHTNVRDIPYLGTSIQ 600  
 Qy 601 AFPPNTYVCILRLFLSHNMTRKMFVYQGNSQIQTOKTPLVAACTAHRWQ-YFDP 659  
 Db 601 EFPYNTVFLVLRKFHDICVKEVLIVFSENKDQLGVVKTPUVAACNDNNNAQD 659  
 Qy 660 SFDDVAVFKSKMERSLNRNKATAELKATVSSCBLALGKFFSCCFENDDLAEGVDE 660  
 Db 661 DFDVTFLHFSHMQVLSKYYKATAELOSSQAWSSCCOLALTGIFSSCBERNSDPAEAGVDE 719  
 Qy 720 DEDLTWCLMSKFTADLRPYPFLSPAROFAGMLIELLSDRBHQDGLYHKOIN 779  
 Db 721 DVKLTVFLMSKFTAQRLRVPYRFGLPQEEFLAVRTELASSDQBDQDGLYHKOIN 779  
 Qy 780 SPMMTWSAYNENFLVNUSSLESTRAGPKVLSVHLVNLVNEKELENSENDVYKHOEISL 839  
 Db 781 SPLKAINSNFLFLYVSSKRAPTVHSQHLOQDEKESLLENSENEDYMKLHPQTL 839  
 Qy 840 QMQLLRGMQMCPOAFYSMWVSEHLLVALKTAYQSONNTVAASPFVLOFLOGRTLGA 840  
 Db 841 WFQFVRGLMVLVSPESFVSFVSEHLLRLALITYESTVACSCSPFLQFLRGTLALRYV 899  
 Qy 900 LQYFDHESLRSLRSHTFPPRGKNTSPRAHFSVLAETCFDKSQTPTDODYSAFERME 900  
 Db 901 LEFWDHPESSLRLRSKVINGNKNUSSVYVDS FKTYFENLQPAPAINEEYSAFEHVE 959  
 Qy 950 WERNLAKEKDNVSKYMDMQRASPDLSTGWKLSPKQYKIPCLCDEVNDIDVGQMLEI 959  
 Db 960 WRRNAQADEETIKNYENIWPRLPDISEYWNUSSPKPKCIPKIPLEVQVNMGADQQLV 1019  
 Qy 1020 LMVFSASORIELHUNHSRGGFESTRPALELSKASVTKCSTSKELELSAEQELULITPL 1079  
 Db 1020 LMVFSASOSIEFHNFSSGFLTESTRPALELSKASVTKCSTSKELELSAEQELULITPL 1079  
 Qy 1080 ESLEYSGTOSQDQFLPNKDPUKLUCKIHSVDEBGNINVFSYIPEEPNFHHMEKLIQS 1139  
 Db 1080 OSLEYSETNQDOPDOLFHNLHKFLGLKSLCVRDGLKPVLSPVLEEPUNLHMEKLIQS 1139  
 Qy 1140 AEYPSKLMKLLQNSPQNLJFHKCNFNSFDSFGSLMMVLVSKKLTTEIKSDSTFOAVPV 1199  
 Db 1140 TESDLSKLVQFLONFPNLHFLKCPULSNCESLMTALASCKLKREIFSGOCPEAMFV 1199  
 Qy 1200 ASLNFISKUJLNLLEGQFDPDESETFAYFGLSISNBLPLPTGDSYRALKLITQ 1259  
 Db 1200 NLNFNVLSKLISLKGQOFANKETSEKFAQGLSRLNLBLLVPMGDCIHOKAKLVRQ 1259  
 Qy 1260 QDHCILWLSFKTLLNDSSVVEAKVATSGFQLLENKLSTHKKTEEGTRNFFALDN 1319  
 Db 1260 QDHCILWLSFKTLLNDSSVVEAKVATSGFQLLENKLSTHKKTEEGTRNFFALDN 1319  
 Qy 1320 MPNQELDISRHFTCEICKAORTVKSLSQCVLPLRILNMSWLDAADDIALJAVMK 1379  
 Qy 1319 LFLNQMLNCRNPRGIOQVATWVKALCHCVRSLPLSLRGLMSLWLDEDMKVVINDKE 1379  
 Qy 1380 RHPQSKYLTILQKWLPSPI 1401  
 Db 1379 RHPQSKRLTFLWMKIVPSPV 1400

RESULT 7  
 CARC\_HUMAN

ID CARC\_HUMAN STANDARD; PRT: 1024 AA.  
 AC Q9NP4; Q96J83; Q96Q82; Q96Q81; -.  
 DT 01-MAR-2002 (Rel. 41, last sequence update)  
 DT 01-MAR-2002 (Rel. 41, last annotation update)  
 DE Caspase recruitment domain protein 12 (ice-protease activating factor) (IpaF) (CARD, LRR, and NACHT-containing protein) (Clan protein).  
 DE CARD12 OR CLAN1 OR CLAN.  
 GN Homo sapiens (Human).  
 OC Burkヨota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1] SEQUENCE FROM N.A. (ISOFORM 1).  
 RP MEDLINE-21265963; PubMed-117474873;  
 RA Geddes B.J., Wang L., Huang W.-J., Lavellee M., Manji G.A., Brown M., Jurman M., Cao J., Morrenstern J., Merriam S., Glucksmann M.A., Di Stefano P.S., Bertin J.;  
 RA "Human CARD12 is a novel CED4/Apaf-1 family member that induces apoptosis";  
 RL Biochem. Biophys. Res. Commun. 284:77-82(2001).  
 RN [2] SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).  
 RC TISSUE=Lung;  
 RX Pubmed=11472070;  
 RA Damiano J.S., Steinlik C., Pio F., Godzik A., Reed J.C.;  
 RT Genomics 75:77-83(2001).  
 RL [3] SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Leukocyte;  
 RX Published=11390368;  
 RA Poyet J.-L., Srinivasula S.M., Tsanis M., Razmara M., Fernandes-Alnemri T., Alnemri E.S.;  
 RT "Identification of IpaF, a human caspase-1-activating protein related to Apaf-1";  
 RT J. Biol. Chem. 276:28309-28313(2001).  
 RN [4] SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Giopras M., Otu J., Margolin J.F.;  
 RT "Differential expression of the caspase recruitment domain protein 12 (CARD12) during monocytic differentiation";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [5] SEQUENCE OF 586-1024 FROM N.A. (ISOFORM 1).  
 RA Aufray C., Ansorge W., Ballabio A., Estivill X., Gibson K., Lehach H., Pousta A., Lundberg J.,  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 CC -- FUNCTION: Plays a role in the promotion of apoptosis.  
 CC -- SUBUNIT: Self associates and binds to ASC, pro-caspase-1, Nod2, BCL10 and NALP1 (NAC) by CARD-CARD interaction.  
 CC -- SUBCELLULAR LOCATION: Cytoplasmic filaments.  
 CC -- ALTERNATIVE PRODUCTS: 4 isoforms, 1/CLAN1 (shown here), 2/CLANB, 3/CLANC and 4/CLAND; are produced by alternative splicing.  
 CC -- TISSUE SPECIFICITY: Isoform 2 is expressed ubiquitously, although highly expressed in lung and spleen. Isoform 1 is highly expressed in lung, followed by leukocytes especially monocytes, lymph node, colon, brain, prostate, placenta, spleen, bone marrow and fetal liver. Isoform 4 is only detected in brain.  
 CC -- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -- SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
 CC -- SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).

DR EMBL: AY027788; AAK14777.1; -.  
 DR EMBL: AY027789; AAK14778.1; -.  
 DR EMBL: AY027790; AAK14779.1; -.  
 DR EMBL: AY035391; AAK53843.1; -.  
 DR EMBL: AF376061; AAK53443.1; -.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS5037; NACHT; 1.  
 KW Apoptosis; ATG-binding; Repeat; Leucine-rich repeat;  
 KW Alternative splicing.  
 FT DOMAIN 1 88  
 FT NP\_039136 163 476  
 FT NP\_039136 169 176  
 FT REPEAT 7 30  
 FT REPEAT 258 281  
 FT REPEAT 578 598  
 FT REPEAT 656 679  
 FT REPEAT 735 758  
 FT REPEAT 752 785  
 FT REPEAT 787 812  
 FT REPEAT 824 847  
 FT REPEAT 848 870  
 FT REPEAT 878 902  
 FT REPEAT 911 933  
 FT REPEAT 936 963  
 FT REPEAT 965 985  
 FT REPEAT 999 1021  
 FT VARSPLC 89 753  
 FT VARSPLC 155 156  
 FT VARSPLC 157 1024  
 FT VARSPLC 90 92  
 FT VARSPLC 93 1024  
 FT CONFLICT 138 138  
 FT CONFLICT 393 393  
 FT CONFLICT 420 420  
 FT CONFLICT 678 678  
 SQ SEQUENCE 1024 AA; 116158 MW; 49378DBB54938E0F CRC64;

Query Match 8 9%; Score 654; DB 1; Length 1024;  
 Best Local Similarity 23.7%; Pred. No. 3.5e-31; Gaps 42;  
 Matches 263; Conservative 197; Mismatches 410; Indels 238; Gaps 42;

Oy 344 FLQNNMS-SAEVTPLQLSGELCELETTSESNELESDIASIVGPIVPEMAQEAQWFOEAKN 402  
 ||::| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||  
 Db 69 FLSKSEWNTPLQFQDLNGO---SLFHQSEGDD---- 100  
 Oy 403 LNEQLRAAVTISASFRMISLIDDISSLATDHLGCDLSI--ASHKISKV----- 449  
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 101 LAQDQKLWHTPSFLN-----YPLGEDIDIFNLKSTTFEVLRKDQHHR 148  
 Oy 450 QEPYLVEPEVGNLNSVMCYPEGEAGSKTVLUKKTAFLWASGCCUINRQPVLFSLST 509  
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||  
 Db 149 VEQLTINGLQLAQALASPCTIEGESEKGKSTLQRMLWNGKCALTKKFVFLRLS-- 206  
 Oy 510 RPDEGLASLICDQLEKEGSYTEMCMRNITQQLKNQVLFDDYKIECSIPQ---VIGL 566  
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||  
 Db 207 RAQGGLFETLQDQLDIPGTIRKOFFMAMLKURQVLFLDGNEF-KPQNCPPEIEAL 264  
 Oy 567 IOKNHLRSRCLLIAVTRNRDIRRYLETILEIKAPFPFTVCIRKLFSHNMRKEM 626  
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||  
 Db 265 IKENHRFKNMIVITTECLRHROFGALTAEVGMTEASAQALIREVILKELA--EGLL 322  
 Oy 627 VYFGKQNSLRIQKPLFWVATICAHMWFQYFPDPSPDDVAVPKSYMERUSLRNK----A 680  
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||  
 Db 323 LQIQSRSCRLNIMKTPFLWVTCIAQMGSSEFSHSTQTTLFHTYDLLIQNKKHKGVA 382  
 Oy 681 TAEILKATVSSCGELAKGFFSCCEFNFDDLAEGYDDEDLMCLMSKFTAOQLRPFY 740  
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||  
 Db 383 ASDFR-SLDHGCLALEGVFSHKDFELQDV--SSVNBDVLUFTGLCKYTAORPKY 439  
 Oy 741 RFLSPAFAQFPLLAGMLIELPDSRHOHQDLYHIQKQIPMMTVSAVHNFLNVV--SSL 798  
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||

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DR EMBL: AY027787; AAK14776.1; -.

Db	440 KFPFHRSQFOETTAGRRLSSLTSRHEPEEVTKGNGYLOKWNISIDITYSSLRTYCGSSV	499
Qy	799 PSTKAGPKTVSHLHLHLDN-----KESLEIISENDYLUKHPEIQLQNL	843
Db	500 EATRA---WVKHLAVVWQHGCLGLSLTAKPLWRBLSQSVN-----TTQEI	545
Qy	844 LRGWQICPQAYPSMVSEHLLVLAUKTAYQSNT-VAACSFVLFQFLGRTLTGALNL-Q	901
Db	545 LKAI---NINSFVECGIHL-----YQESTKSALSQEEFAFFOCKSLYNSNPD	593
Qy	902 YFDHPESLLRSIHSPIGRNKTSPRAHESVLETCDFDKSQTVDYASAFEPNWE	961
Db	594 YLFD-----FPEHLPNC-A-SALDFIKLDFYCG-AMASNE	625
Qy	962 RMLAEKEDNVKSYMDQMRRSPDLSTGFWKLSPKQYKIP-----CLEVDV	1006
Db	626 -----KAEDTGIIIMEAPTY-IPSRAVSLPFNNWQKQFRTEVLT	666
Qy	1007 NDIDVGQDMLEIATMVTSAQRIEHLHNSGKFPLSASKYTKCSISLKS	1066
Db	667 RDFSRLANKODIRYLGKIFSSATSLRQIKRAGVAGSLSLWSTICK-NIYSLAAVEASPLT	1124
Qy	1067 AAEGLLITLPLSLESLEVSGTQSOPQIFPN-LDKFLCLKEVSVDLGNINIVSVPPE	725
Db	726 IEDERHHSVTNUKTLSIH--DLQMQRLGGUDSIGNKNTKLMDNM-----	775
Qy	1125 FPNFHMHMRKLQIISAEYDPKSKVLQIIONSPNLHVPHKCNFSDGCSLMMLMVS---	1179
Db	776 -----NEEDAIIKLAGBLKNIKMKHCLPHL-TILSDIGEGMDYIVKSLSE	818
Qy	1180 -OKKLBIKESDSFF-QAQPVFA-SLNFISIKLIMLEGQOFDEDESTEKFAYLGSIS	1235
Db	819 PC-DLEIQQWSCCUSANAVKTLAQNLNLVVKLISLSDL-SINYLKDGNEALHLDIQRN	1235
Qy	1236 NLEE---LITPTGQIYRVALIQQOQLHCLRVSSFFKTLDDSVELAKAISGCF-	876
Db	877 VLEOLTAALMPPGCDVOGLSSLLKHLLEEVPOLVKGKLNWKRLTDY-----ERILGAFF	1291
Qy	1347 SQCVRLRPLRILNLMSWLADDIYL 1374	987
Db	988 SONYSLKJTFQGBARRWQHDDDSLVI 1015	
RESULT	9	
BIR3_HUMAN		
ID	BIR3_HUMAN STANDARD;	
AC	O13490; Q16516;	
DT	01-NOV-1997 (Rel. 35, last sequence update)	
DT	16-OCT-2001 (Rel. 40, last annotation update)	
DE	Baculovirus IAP repeat-containing Protein 3 (Inhibitor of apoptosis protein 2) (IAP2) (IAPB-2) (C-IAP1) (TNFR2-TRAF signaling complex protein 2) (IAP homolog B), BIRC3 OR API2 OR IAP2 OR MIH.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX	
RN	[1] NC_001045;	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=96128127; PubMed=8558810;	
RA	Pothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;	
RT	*The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.	
RL	Cell 83:1243-1252(1995).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	LINE=95149249; PubMed=8552191;	
RA	Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G., Paralani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.; "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.", Nature 379:349-353(1996).	
RT	[3]	
RL	SEQUENCE FROM N.A.	
RN	TISSUE=Fetal liver;	
RC		
RX	Medline=96209843; Pubmed=8643514;	
RA	Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.; "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.", Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).	
RT	"Solution structure of a baculoviral inhibitor of apoptosis (IAP) with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to recruit the tumor necrosis factor receptor 2 (TNFR2).", Nat. Struct. Biol. 6:648-651(1999).	
RL	- - FUNCTION: Apoptotic suppressor.	
CC	STRUCTURE BY NMR OF 266-363.	
CC	WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROGENIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).	
CC	- - SIMILARITY: Contains 3 CARD DOMAINS.	
CC	- - TISSUE SPECIFICITY: Present in many fetal and adult tissues.	
CC	MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY, AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD.	
CC	LEUKOCYTES.	
CC	- - SIMILARITY: BELONGS TO THE IAP FAMILY.	
CC	- - SIMILARITY: Contains 3 BIR REPEATS.	
CC	- - SIMILARITY: CONTAINS 1 CARD DOMAIN.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	
DR	EMBL; L49431; AAC41942.1;	
DR	EMBL; U5879; AAC50372.1;	
DR	EMBL; U31547; AAC50508.1; -	
DR	MIM: 601721; -	
DR	InterPro: IPR01370; BIR.	
DR	InterPro: IPR01315; CARD.	
DR	InterPro: IPR01841; Znf_Ring.	
DR	Pfam: PF00653; BIR; 3.	
DR	Pfam: PF00619; CARD; 1.	
DR	Pfam: PF00097; zf-C3HC4; 1.	
DR	SMART: SM00238; BIR; 3.	
DR	SMART: SMART; SM0014; CARD; 1.	
DR	PROSITE: PS00184; RING; 1.	
DR	PROSITE: PS01282; BIR_REPEAT_1; 3.	
DR	PROSITE: PS50209; CARD; 1.	
DR	PROSITE: PS00518; ZF_RING_1; FALSE_NEG.	
KW	PROSITE; PS50089; ZF_RING_2; 1.	
FT	Apoptosis; Zinc-finger; Repeat; 3D-structure.	
FT	REPEAT 46 113 BIR 1.	
FT	REPEAT 184 250 BIR 2.	
FT	REPEAT 269 335 BIR 3.	
FT	DOMAIN 453 543 CARD.	
FT	ZN_FING 571 606 RING_TYPE.	
FT	REPEAT 308 S > P (IN REF. 2).	
FT	CONFFLICT 414 Q -> L (IN REF. 2).	
FT	CONFFLICT 514 L -> W (IN REF. 2).	
SQ	SEQUENCE 618 AA; 69899 MW; C17780328003586D C1C64;	

Query Match	6.3%	Score 462; DB 1; Length 618;
Best Local Similarity	26.0%	Pred. No. 4.2e-20; Indels 146; Gaps 22;
Matches	155;	Conservative 82; Mismatches 214; Delins 146; Gaps 22;
1	LEEKEEAKERAKNQKGNSQMRSEAKRLKTFVTEPYSSWIP--QEMAAGFVFIGVKG 94	R1
2	LSDWTNSNKOKYKDYDSE--LRYMSTYSTEPAVGVPERSLARGFYTGVDK 80	R1
3	IQCFCCLSLIFGAGLTLRPIEDHKRFHDGCF--LINKDVGNTAKYDIRVKN----- 144	Genomics 49:5-503(1997).
4	IQCFCCLSLIFGAGLTLRPIEDHKRFHDGCF--LINKDVGNTAKYDIRVKN----- 144	-1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROmeric COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).
5	IQCFCCLSLIFGAGLTLRPIEDHKRFHDGCF--LINKDVGNTAKYDIRVKN----- 144	-1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
6	IQCFCCLSLIFGAGLTLRPIEDHKRFHDGCF--LINKDVGNTAKYDIRVKN----- 144	-1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
7	IQCFCCLSLIFGAGLTLRPIEDHKRFHDGCF--LINKDVGNTAKYDIRVKN----- 144	-1- SIMILARITY: BELONGS TO THE IAP FAMILY.
8	WKCFCGGLMLDNWKLGSPDKHQLQPLSCSFIONLISASLGTSKNTSPMRNFAHSLS 140	-1- SIMILARITY: CONTAINS 3 BIR REPEATS.
9	WKCFCGGLMLDNWKLGSPDKHQLQPLSCSFIONLISASLGTSKNTSPMRNFAHSLS 140	-1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
10	WKCFCGGLMLDNWKLGSPDKHQLQPLSCSFIONLISASLGTSKNTSPMRNFAHSLS 140	CC
11	LKSRL-----RGKMKY--QEEEARLASFRNWPFFYVQ 175	CC
12	PTLEHSSLFSGSYSSLSPNPLNSRAVEDISSRTNPYSYAMSTMESTEARFLTYHKWP-LTF 198	CC
13	ISPCVULSEAGFVFTGKODTQFCFSGCGLGNGWEQDPWKKHAKWPKCEFLSKSSEE 235	CC
14	ISPCVULSEAGFVFTGKODTQFCFSGCGLGNGWEQDPWKKHAKWPKCEFLSKSSEE 235	CC
15	ISPCVULSEAGFVFTGKODTQFCFSGCGLGNGWEQDPWKKHAKWPKCEFLSKSSEE 235	CC
16	ISPCVULSEAGFVFTGKODTQFCFSGCGLGNGWEQDPWKKHAKWPKCEFLSKSSEE 235	CC
17	ISPCVULSEAGFVFTGKODTQFCFSGCGLGNGWEQDPWKKHAKWPKCEFLSKSSEE 235	CC
18	ISPCVULSEAGFVFTGKODTQFCFSGCGLGNGWEQDPWKKHAKWPKCEFLSKSSEE 235	CC
19	ISPCVULSEAGFVFTGKODTQFCFSGCGLGNGWEQDPWKKHAKWPKCEFLSKSSEE 235	CC
20	ISPCVULSEAGFVFTGKODTQFCFSGCGLGNGWEQDPWKKHAKWPKCEFLSKSSEE 235	CC
21	ISPCVULSEAGFVFTGKODTQFCFSGCGLGNGWEQDPWKKHAKWPKCEFLSKSSEE 235	CC
22	ISPCVULSEAGFVFTGKODTQFCFSGCGLGNGWEQDPWKKHAKWPKCEFLSKSSEE 235	CC
23	ITQYQSYKGFVDTGEHFVNNSWQRELPMASAYCNDISAYEELRUDSFKDWPRESAV 295	CC
24	ITQYQSYKGFVDTGEHFVNNSWQRELPMASAYCNDISAYEELRUDSFKDWPRESAV 295	CC
25	TURFSIS-----NLSMOT-----HAARMYTFMYKPSSVYQ 286	CC
26	VAALAKAGLFVNGIKDIVQCSGGGLEKWKQSEGDPDPLDPHTRCFPNCPPFLQHQSAAEV 355	CC
27	PEQLASAGFVYVGRNDWDVKFCGCGGLRCWESGDDPWPVHEAKWPKCEFLRMKGQ-EFV 345	CC
28	PEQLASAGFVYVGRNDWDVKFCGCGGLRCWESGDDPWPVHEAKWPKCEFLRMKGQ-EFV 345	CC
29	PDLQSR_GELCELLETSSENLEDSDIAVGPPIPPEMAOEQAOWQEAQNLENEOLRAYSA 414	CC
30	PDLQSR_GELCELLETSSENLEDSDIAVGPPIPPEMAOEQAOWQEAQNLENEOLRAYSA 414	CC
31	DEBQIOPHRPHLQLLSDPSDTGEGE--ADPPITHFGCGES-SEDAVNMNTPVKALEM 402	CC
32	SPHRMSLSDISSLATDHLLGCOLSDIASKHKISHPKVQEP-LVLPEVFGNLNSVMCVEGEM 473	CC
33	SPHRMSLSDISSLATDHLLGCOLSDIASKHKISHPKVQEP-LVLPEVFGNLNSVMCVEGEM 473	CC
34	SPHRMSLSDISSLATDHLLGCOLSDIASKHKISHPKVQEP-LVLPEVFGNLNSVMCVEGEM 473	CC
35	GFRN-----DL-----VKQTQSLTITIGENYKVNDIYALLMAE 438	CC
36	GFRN-----DL-----VKQTQSLTITIGENYKVNDIYALLMAE 438	CC
37	SGKTVLK-KIAFLWASGCCPLNRFQVFLSLSSTRPDEGLASICDQOLLERKEGSVTE 532	CC
38	SGKTVLK-KIAFLWASGCCPLNRFQVFLSLSSTRPDEGLASICDQOLLERKEGSVTE 532	CC
39	DEKREKEEKQAEAMASDDLSLIRKNMALFOOLTCVLP-----ILDNLK----- 484	CC
40	DEKREKEEKQAEAMASDDLSLIRKNMALFOOLTCVLP-----ILDNLK----- 484	CC
41	533 MCMMNIQIQQLKQVFLFLDDYYKRICKSIPQVIGLIQKWHHLRSCLLIAVRNARDI 589	CC
42	533 MCMMNIQIQQLKQVFLFLDDYYKRICKSIPQVIGLIQKWHHLRSCLLIAVRNARDI 589	CC
43	485 --ANVINKQEHII-----KOKTOQIPLQARELID-----TILVGNNAANI 523	CC
44	485 --ANVINKQEHII-----KOKTOQIPLQARELID-----TILVGNNAANI 523	CC
45	RESULT 9	RT
46	BIR3_MOUSE STANDARD: PRT: 612 AA.	R1
47	01-NOV-1997 (Rel. 35, Created)	R1
48	01-NOV-1997 (Rel. 35, Last sequence update)	R1
49	16-OCT-2001 (Rel. 40, Last annotation update)	R1
50	Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 2) (MAP-2) (MAP-2).	R1
51	Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 2) (MAP-2). (MAP-2).	R1
52	MUS musculus (Mouse).	R1
53	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	R1
54	NCBI_TaxID=10090;	R1
55	[1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
56	RP MEDLINE-96128127; Pubmed=8848810;	R1
57	Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.; "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins." Cell 83:1243-1252(1995).	R1
58	RP SEQUENCE FROM N.A.	R1
59	TISSUE-Skeletal muscle;	R1
60	LINE 9810590; Pubmed=9441758;	R1
61	Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; R1	R1
62	106 062210; 008864;	R1
63	AC 4C	R1
64	DT 01-NOV-1997 (Rel. 35, Created)	R1
65	DT 01-NOV-1997 (Rel. 35, Last sequence update)	R1
66	DT 16-OCT-2001 (Rel. 40, Last annotation update)	R1
67	DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 2) (MAP-2) (MAP-2).	R1
68	DE Protein 3 (Inhibitor of apoptosis protein 2) (MAP-2).	R1
69	DE BIR3 OR API2 OR IAP2.	R1
70	DOC BIR3C OR API2 OR IAP2.	R1
71	DOC MUS musculus (Mouse).	R1
72	DOC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	R1
73	DOC NCBI_TaxID=10090;	R1
74	DP [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
75	RP SEQUENCE FROM N.A.	R1
76	Query Match	RT
77	Best Local Similarity	R1
78	Matches	R1
79	148; Conservative 73; Mismatches 207; Indels 129; Gaps 19;	R1
80	07 01-NOV-1997 (Rel. 35, Last sequence update)	R1
81	07 16-OCT-2001 (Rel. 40, Last annotation update)	R1
82	07 BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
83	07 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
84	07 DOC BIR3C OR API2 OR IAP2.	R1
85	07 MUS MUSCULUS (MOUSE).	R1
86	07 EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUROTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	R1
87	07 NCBI_TAXID=10090;	R1
88	07 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
89	07 RP MEDLINE-96128127; Pubmed=8848810;	R1
90	07 Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.; "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins." Cell 83:1243-1252(1995).	R1
91	07 RP SEQUENCE FROM N.A.	R1
92	07 TISSUE-Skeletal muscle;	R1
93	07 LINE 9810590; Pubmed=9441758;	R1
94	07 Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; R1	R1
95	07 106 062210; 008864;	R1
96	07 AC 4C	R1
97	07 DT 01-NOV-1997 (Rel. 35, Created)	R1
98	07 DT 01-NOV-1997 (Rel. 35, Last sequence update)	R1
99	07 DT 16-OCT-2001 (Rel. 40, Last annotation update)	R1
100	07 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
101	07 DE PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
102	07 DOC BIR3C OR API2 OR IAP2.	R1
103	07 MUS MUSCULUS (MOUSE).	R1
104	07 EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUROTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	R1
105	07 NCBI_TAXID=10090;	R1
106	07 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
107	07 RP SEQUENCE FROM N.A.	R1
108	07 TISSUE-Skeletal muscle;	R1
109	07 LINE 9810590; Pubmed=9441758;	R1
110	07 Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; R1	R1
111	07 106 062210; 008864;	R1
112	07 AC 4C	R1
113	07 DT 01-NOV-1997 (Rel. 35, Created)	R1
114	07 DT 01-NOV-1997 (Rel. 35, Last sequence update)	R1
115	07 DT 16-OCT-2001 (Rel. 40, Last annotation update)	R1
116	07 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
117	07 DE PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
118	07 DOC BIR3C OR API2 OR IAP2.	R1
119	07 MUS MUSCULUS (MOUSE).	R1
120	07 EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUROTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	R1
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122	07 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
123	07 RP SEQUENCE FROM N.A.	R1
124	07 TISSUE-Skeletal muscle;	R1
125	07 LINE 9810590; Pubmed=9441758;	R1
126	07 Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; R1	R1
127	07 106 062210; 008864;	R1
128	07 AC 4C	R1
129	07 DT 01-NOV-1997 (Rel. 35, Created)	R1
130	07 DT 01-NOV-1997 (Rel. 35, Last sequence update)	R1
131	07 DT 16-OCT-2001 (Rel. 40, Last annotation update)	R1
132	07 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
133	07 DE PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
134	07 DOC BIR3C OR API2 OR IAP2.	R1
135	07 MUS MUSCULUS (MOUSE).	R1
136	07 EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUROTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	R1
137	07 NCBI_TAXID=10090;	R1
138	07 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
139	07 RP SEQUENCE FROM N.A.	R1
140	07 TISSUE-Skeletal muscle;	R1
141	07 LINE 9810590; Pubmed=9441758;	R1
142	07 Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; R1	R1
143	07 106 062210; 008864;	R1
144	07 AC 4C	R1
145	07 DT 01-NOV-1997 (Rel. 35, Created)	R1
146	07 DT 01-NOV-1997 (Rel. 35, Last sequence update)	R1
147	07 DT 16-OCT-2001 (Rel. 40, Last annotation update)	R1
148	07 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
149	07 DE PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
150	07 DOC BIR3C OR API2 OR IAP2.	R1
151	07 MUS MUSCULUS (MOUSE).	R1
152	07 EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUROTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	R1
153	07 NCBI_TAXID=10090;	R1
154	07 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
155	07 RP SEQUENCE FROM N.A.	R1
156	07 TISSUE-Skeletal muscle;	R1
157	07 LINE 9810590; Pubmed=9441758;	R1
158	07 Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; R1	R1
159	07 106 062210; 008864;	R1
160	07 AC 4C	R1
161	07 DT 01-NOV-1997 (Rel. 35, Created)	R1
162	07 DT 01-NOV-1997 (Rel. 35, Last sequence update)	R1
163	07 DT 16-OCT-2001 (Rel. 40, Last annotation update)	R1
164	07 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
165	07 DE PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
166	07 DOC BIR3C OR API2 OR IAP2.	R1
167	07 MUS MUSCULUS (MOUSE).	R1
168	07 EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUROTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	R1
169	07 NCBI_TAXID=10090;	R1
170	07 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
171	07 RP SEQUENCE FROM N.A.	R1
172	07 TISSUE-Skeletal muscle;	R1
173	07 LINE 9810590; Pubmed=9441758;	R1
174	07 Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; R1	R1
175	07 106 062210; 008864;	R1
176	07 AC 4C	R1
177	07 DT 01-NOV-1997 (Rel. 35, Created)	R1
178	07 DT 01-NOV-1997 (Rel. 35, Last sequence update)	R1
179	07 DT 16-OCT-2001 (Rel. 40, Last annotation update)	R1
180	07 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
181	07 DE PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
182	07 DOC BIR3C OR API2 OR IAP2.	R1
183	07 MUS MUSCULUS (MOUSE).	R1
184	07 EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUROTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	R1
185	07 NCBI_TAXID=10090;	R1
186	07 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
187	07 RP SEQUENCE FROM N.A.	R1
188	07 TISSUE-Skeletal muscle;	R1
189	07 LINE 9810590; Pubmed=9441758;	R1
190	07 Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; R1	R1
191	07 106 062210; 008864;	R1
192	07 AC 4C	R1
193	07 DT 01-NOV-1997 (Rel. 35, Created)	R1
194	07 DT 01-NOV-1997 (Rel. 35, Last sequence update)	R1
195	07 DT 16-OCT-2001 (Rel. 40, Last annotation update)	R1
196	07 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
197	07 DE PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
198	07 DOC BIR3C OR API2 OR IAP2.	R1
199	07 MUS MUSCULUS (MOUSE).	R1
200	07 EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUROTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	R1
201	07 NCBI_TAXID=10090;	R1
202	07 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
203	07 RP SEQUENCE FROM N.A.	R1
204	07 TISSUE-Skeletal muscle;	R1
205	07 LINE 9810590; Pubmed=9441758;	R1
206	07 Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; R1	R1
207	07 106 062210; 008864;	R1
208	07 AC 4C	R1
209	07 DT 01-NOV-1997 (Rel. 35, Created)	R1
210	07 DT 01-NOV-1997 (Rel. 35, Last sequence update)	R1
211	07 DT 16-OCT-2001 (Rel. 40, Last annotation update)	R1
212	07 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
213	07 DE PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
214	07 DOC BIR3C OR API2 OR IAP2.	R1
215	07 MUS MUSCULUS (MOUSE).	R1
216	07 EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUROTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	R1
217	07 NCBI_TAXID=10090;	R1
218	07 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
219	07 RP SEQUENCE FROM N.A.	R1
220	07 TISSUE-Skeletal muscle;	R1
221	07 LINE 9810590; Pubmed=9441758;	R1
222	07 Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; R1	R1
223	07 106 062210; 008864;	R1
224	07 AC 4C	R1
225	07 DT 01-NOV-1997 (Rel. 35, Created)	R1
226	07 DT 01-NOV-1997 (Rel. 35, Last sequence update)	R1
227	07 DT 16-OCT-2001 (Rel. 40, Last annotation update)	R1
228	07 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
229	07 DE PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
230	07 DOC BIR3C OR API2 OR IAP2.	R1
231	07 MUS MUSCULUS (MOUSE).	R1
232	07 EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUROTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	R1
233	07 NCBI_TAXID=10090;	R1
234	07 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
235	07 RP SEQUENCE FROM N.A.	R1
236	07 TISSUE-Skeletal muscle;	R1
237	07 LINE 9810590; Pubmed=9441758;	R1
238	07 Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; R1	R1
239	07 106 062210; 008864;	R1
240	07 AC 4C	R1
241	07 DT 01-NOV-1997 (Rel. 35, Created)	R1
242	07 DT 01-NOV-1997 (Rel. 35, Last sequence update)	R1
243	07 DT 16-OCT-2001 (Rel. 40, Last annotation update)	R1
244	07 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
245	07 DE PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MAP-2).	R1
246	07 DOC BIR3C OR API2 OR IAP2.	R1
247	07 MUS MUSCULUS (MOUSE).	R1
248	07 EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUROTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	R1
249	07 NCBI_TAXID=10090;	R1
250	07 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	R1
251	07 RP SEQUENCE FROM N.A.	R1
252	07 TISSUE-Skeletal muscle;	R1
253	07 LINE 9810590; Pubmed=9441758;	

Db 251 RES-----ISNLSMOTHSARLRTFLYWPSPV 278  
 Qy 295 GVAALAKAGLYFTGKIDIVOCPSGGCLEKWKQGDDPRDHRCFPCPQELQNMSSAEV 354  
 Db 279 OPEQLASAGAFYVYDRNDVKFCFCGCGURCKEGGDWMIERAKWFRCEEFIRMIGQ-EF 337  
 Qy 355 TPDQSR-GCLCELETTSESNLIEDSIAVGTIVPEMAQEAQWFQAQNLEONLRAVYS 413  
 Db 338 VDEIOARYPHULOLSTSDTPEGENADPTETVHFGPE-----SS 379  
 Qy 414 ASFRIMSLIDLISSOLATDHLGLDSLASKHISKPKOEPVLPVEFGNINSMCV---E 469  
 Db 380 EDVMMSTPVKALE---MCFRSNLVQRTVQROI---LATGENYRTVNDIVSULNAE 432  
 Qy 470 GEAGSKGVKLKKIAFWASGCCPLNRFQLVFLSLSSTRPDEGLASTICDOLLEREGS 529  
 Db 433 DERREEK--BROTEMASDGLSLRKNMALFOOLTHVL-----ILDNLL-EAS 480  
 Qy 530 VTNCMNICITOLKNQ 546  
 Db 481 VTKQEHDIHQ-KTOI 496

RESULT 10

BIR2\_MOUSE STANDARD; PRT; 600 AA.  
 AC 008863;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Baculoviral IAP repeat-containing protein 1 (Inhibitor of apoptosis protein 1) (MAP1) (MAP-1).  
 GN BIRC2 OR Apaf OR IAPI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OX NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N A.  
 RX MEDLINE=98110590; PubMed=9441758;  
 RA Liston P.; Lefebvre C.; Fong W.G.; Xuan J.Y.; Korneluk R.G.;  
 RT Genomic characterization of the mouse inhibitor of apoptosis protein 1 and 2 genes.;  
 RL Genomics 46:493-503(1997).  
 CC FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS FORM AN HETEROGENERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).  
 CC -.- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -.- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -.- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -.- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -.- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@ibb-sib.ch).  
 DR EMBL; U88908; AAC55531.1; -.  
 DR HSSP; Q13490; IQBH  
 DR MGD; MG1-1197007; Birc2.  
 DR InterPro; IPR001370; BIR.  
 DR InterPro; IPR001315; CARD.  
 DR Pfam; PF00653; BIR; 3.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00097; zf-C3H4; 1.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS01013; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS50518; ZF\_RING\_1; FALSE\_NEG.  
 KW Apoptosis; Zinc\_finger; Repeat.  
 FT REPEAT 27 94  
 FT REPEAT 167 233  
 FT REPEAT 253 320  
 FT DOMAIN 435 525  
 FT ZN\_FING 553 588  
 SQ 600 AA; 67198 MW; AD7F73E6849317D1 CRC64;

Query Match 6.0%; Score 440; DB 1; Length 600;  
 Best Local Similarity 23.3%; Pred. No. 8.2e-19; Matches 145; Conservative 88; Mismatches 226; Index 162; Gaps 19;

Db 9 AKMOKGNS---QNSKEAKRLKPFVTFYQSCENYRSL---TYSAFPRGVPSERSLARGFYVKGKSIQCF 98  
 Qy 99 CCSLILFGAGLTRLPIEDKRFHDGCGLLNKVGNIAKYDTRVNLKSRRGGRMRY -- 156  
 Db 66 CGGLMLDNWNRQGDSPPMKEHRKLYPSCNFQVTLNPANSLESAPPSPUPSTAMIAHPLSFAS 125  
 Qy 157 -----GEEARLASFNWRPYDGS 177  
 Db 126 SENTGYFCSYSSFPSPDVNFANQDCPALSTSPYHFMATEKARLUTETWP--LSFLS 183  
 Qy 178 PCVSEAGEVTFTQDTCFQCCGGCIGNREPGDPWPWKAHWPKPCERLRSKSSBEIT 237  
 Db 184 PAKLAKAGLYVIGPDRVACACDGKLSNNRKDAMSHQRAHPSCFPLKQGOS --- 239  
 Qy 238 QYIQSYKGFDITGEHEVNSWORELPMASACYNSI-PAYEELRDPSFKDPREAVG 296  
 Db 240 -----ASRYTVNSLNSMOTHSARLRTFLYWPSPV 278  
 Qy 297 ALAKAGLYFTGKIDIVOCPSGGCLEKWKQGDDPRDHRCFPCPQELQNMSSAEV 354  
 Db 272 QELASAGLYFTGKIDIVOCPSGGCLEKWKQGDDPRDHRCFPCPQELQNMSSAEV 356  
 Qy 357 DLQSGRELCELETTSESNLIEDSIAVGTIVPEMAQEAQWFQAQNLEONLRAVYS 413  
 Db 332 VQAGYPHFLQELLSITSDP-EDENADAAVHFGPGESSEDVMSIPVKAENGFS 390  
 Qy 401 --'KLNQEOLAA---YTSASRHMSLIDISDL-----ATDHLGCDLSTASKHISK 447  
 Db 391 LVRTVORGILAGTCNTRVSLVIGLIDAREMREOMEOABEESDLDLARKNMV 450  
 Qy 448 PWQ-PLVLF-VEGNLNNSVMCVMCEAGSKGVKLKKIAFWASGCCPLNRFOLVFSL 506  
 Db 451 LFQHLCYTPMVCYLSSRATTEOECAVNAV----- 480  
 Qy 507 SSTRPDEGLASTICDOLLEKGSVEMCARNIIOOLKNQV--LFLFLDYK---EICS 558  
 Db 481 --QKPHLQASLIDVYLAK-GNTATTSFRNSRREIDPALYRDIFQODIRSLPTDDIAA 537  
 Qy 559 IP--QVIGKLTKORNHLSRCL 577  
 Db 538 LPMEEQQLRL-QEERMCKVCM 557

RESULT 11

BIR2\_HUMAN STANDARD; PRT; 604 AA.  
 ID BIR2\_HUMAN  
 AC Q13490; Q16628; Q04P46;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Baculoviral IAP repeat-containing protein 1 (Inhibitor of apoptosis

DE protein 1) (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF signaling complex  
DE protein 1) (IAP homolog C).  
GN BIRC2 OR API1 OR IAP1 OR MHC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;  
OX NCBI\_TAXID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96128127; PubMed=8518810;  
RA Rotie M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;  
RT "The TNFR2-TRAF signaling complex contains two novel proteins related  
to baculoviral inhibitor of apoptosis proteins.";  
RL Cell 83:1243-1252(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=95149249; PubMed=8552191;  
RA Lisoni P., Roy N., Tamai K., Defeverre C., Chertton-Horvat G.,  
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
family of IAP genes";  
RN Nature 379:349-353(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=96208843; PubMed=8613514;  
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
RT "Cloning and expression of apoptosis inhibitory protein homologs that  
function to inhibit apoptosis and/or bind tumor necrosis factor  
receptor-associated factors";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9252496; Pubmed=10233894;  
RA Horrevorts A.J., Pontijn R.P., van Zonneveld A.J., de Vries C.J.,  
RA ten Cate J.W., Pannekoek H.;  
RT "Vascular endothelial genes that are responsive to tumor necrosis  
factor-alpha in vitro are expressed in atherosclerotic lesions,  
including inhibitor of apoptosis protein-1, stannin, and two novel  
genes";  
RN Blood 93:3418-3431(1999).  
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
FORM AN HETEROERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (Potential).  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN  
THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,  
INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.  
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to license@isb-sib.ch).  
CC

DR Pfam; PF00619; CARD; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR SMART; SM00238; BIR; 3.  
DR SMART; SM00114; CARD; 1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE; PS5043; BIR\_REPEAT\_2; 3.  
DR PROSITE; PS50209; CARD; 1.  
DR PROSITE; PS0518; 2\_RING\_1; FALSE\_NEG.  
DR PROSITE; PS50089; 2F\_RING\_2; 1.  
KW Apoptosis; Zinc-finger; Repeat.  
FT REPORT 29 96  
FT REPAT 169 235  
FT REPAT 255 322  
FT DOMAIN 439 529  
FT ZNFING 557 592  
FT CONFLICT 18 18  
FT CONFLICT 119 119  
FT CONFLICT 153 153  
FT CONFLICT 163 163  
FT CONFLICT 165 165  
FT CONFLICT 191 191  
FT CONFLICT 364 364  
FT CONFLICT 552 552  
FT CONFLICT 604 AA; 68371 MW; 8581AA00BA9A8A7 CRC64;  
SQ SEQUENCE

Query Match 6 0%; Score 436.5; DB 1; Length 604;  
Best Local Similarity 24.5%; Pred. No. 1.3e-18; Mismatches 200; Indels 169; Gaps 22;  
Matches 147; Conservative 84; Mismatches 200; Indels 169; Gaps 22;

QY	69	TYPYSSWIP-----OBMAAGFYPTGYVKSIQOCRCSLIFGAGLULTRLPEDHKRFPHDCG	125
Db	35	TYSTFPAGVPUVSERSLARGFYTYGVNDKVKCFCCGLMLDNWKRGDSPEKKLYPSCR	94
QY	154	--MR-----YQBEEARLASFRNPKPYQIGISCVLSAGEFVFTGKDQDTCFCGGCL	204
Db	126	FLLA-KDVENTI-----AKDIRVNLUKSLSRGK-----	153
QY	95	FVQSLNSVNNELEATSOPTFPPSVNTHSILPGTENSGYFRGSYSNSPSPNVNSRANQDF	154
Db	213	SNWEKDNDAMSEHHLRFKPFQPIEIQ-N-QDTSRKYTV-----NLS	251
QY	265	MASAYCNDISIAYEYLRLSLFKDPRESAVGAVALAKAGLFYNGIKDIVOCFSGGCLEK	324
Db	252	MQT-----HAARFKTFNNPPSVLVNPOLASAGFYVYNSDDVKFCFCDDGLRC	301
QY	325	WQEGDPLDHTRCPNCPPQNLKMSAATVTPDQSLQSRLGCLETTES-----	374
Db	302	WESGDPPWQHAKNPRCCELRKGQEETIROVQASYPPLRQLSTPSGPGENAESSI	361
QY	375	-----NLEDSTAVG-PIVPEMAQGEQWQFQAEKLNQNLRAVATSFRMSLSDIS	425
Db	362	INFERGEDISEDAIMMTIVI-NAAVMFGRSLVKQVORKLATGENR-----LV	413
QY	426	SDLAHDHLLGCDLSTASKLISKPKVOEPYLPEVGNLNSVMCGVEAGESSGTVLLKIAF	485
Db	414	NDLVLQD-LINAEDIEERERERATE-----EKESNDLLIRK--	449
QY	486	LWASGCCPPLNRFQVFYLSLSSTRPDESL-ASTICDQ-----LLER-	526
Db	450	-----NRMALFOHQACVPIVILSDLTAGTINEQHDKVIKOKTOSLOARELITI	499
QY	527	-EGSYTEMCMRN1IQQLK---NOVFLLDDYK---EICSIPOVIGKLQIKNHLSRTC	576
Db	500	LVKGNIAATVFRNSLQEAHVLYFVQDVKYPTEDVSDL--VEEQRLQDEERC	557

DR EMBL; AF070674; AAC683232.1; -.  
DR EMBL; Q3490; IQBHR.  
DR EMBL; U45878; ARCA50371.1; -.  
DR EMBL; U37546; AAC0507.1; -.  
DR EMBL; AF070674; AAC683232.1; -.  
DR InterPro; IPRO01370; BIR.  
DR InterPro; IPRO01315; CARD.  
DR InterPro; IPRO01841; Znf\_fing.  
DR Pfam; PF00653; BIR; 3.



DR Pfam; PF00553; BIR; 3.  
 DR Pfam; PF00097; zf\_C3HC4; 1.  
 DR SMART; SM00238; BIR; 3.  
 DR SMART; SM0014; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS00089; ZF\_RING\_2; 1.  
 KW Apoptosis; zinc-finger; Repeat.  
 FT REPEAT 26 93 BIR 1.  
 REPEAT 163 230 BIR 2.  
 REPEAT 264 329 BIR 3.  
 FT ZN\_FING 449 484 RING\_TYPE.  
 SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;

Query Match 5.7%; Score 416.5; DB 1; Length 496;  
 Best Local Similarity 28.3%; Pred. No. 1..5e-17;  
 Matches 119; Conservative 60; Mismatches 162; Indels 79; Gaps 12;  
 QY 60 EAKSLKTFVTVYEPYSSWQEMAAAGFYFTGVSGIQCFCCSLILFGAGLTRPLIED-- 116  
 Db 26 EFNRLKTFANFPSSSPVSVASTLARAGFLYTGEGDVTVCFSCH----AAVDRMKGDSAV 80

QY 117 --HHRPHDCGFU-----LNKDVGNIAYD 139  
 Db 81 GRHRRISPNCRPFNGFYFENGATQSTSPGQIONGQYKSENCGVNRHNEALDRPSETHADYL 140

QY 140 IR--VKNIKSRURGGKMYQEEARLASFRNPPYVGISPOVULSEAGFVFTGKQDTWQ 196  
 Db 141 LRGQWVVDISDTYPRNPMCSLEARLTQFQNPDYH-LSPRELASGLYVQIDQVQ 199

QY 197 CPGCGCLGNGWECCDDPKEHAWKPKEFLRSKKSSBETIQIQSFKFVDTGEHEVN 256  
 Db 200 CFCGGKLKKNWEPDRAWSEHRHFFPNCPFVLGRN-----VNVRSESGVS 244

QY 257 SWQRELPMSACNDSIFAYEERLDFDKWNRRESAVGVAALAKAGLYFTGKDIYCF 316  
 Db 245 S-DRNFPNSTNSPRNPAMAEYDARIVTGTW--LYSYNQEQLARAGFYVALGBCDKVKCF 300

QY 317 SCGGCLEKWRQEGDDPLDDHTRCFNCPLQNMMSAETPDLSQRLCELETTSE-- 373  
 Db 301 HCCGGLTDMPKPSUPWEDHAKWPGCKYLLDENKGQ-EYINNLILTHSUGESVRTAETP 359

QY 374 --SNLEDSTIAVGPVPEMAQEQWFOEAKNLINEQRLRAYTASFRMSLDDISLAT 430  
 Db 360 SVTKKIDDITFQNPWMQEARIMGFNFKDITKTEBKLO--TSGS-NVLSLEVLIADLV 415

RESULT 14

BIR4\_HUMAN STANDARD; PRT; 497 AA.

ID BIR4\_HUMAN STANDARD; PRT; 497 AA.

AC P91170; O9NQ14; DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein (3) (X-linked inhibitor of apoptosis protein) (X-linked IAP) (IAP-like protein) (HILP), DE BIRC4 OR API3 OR XIAP, DE BIRC4 OR API3 OR XIAP.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606; RN [1].

SEQUENCE FROM N.A.

RC TISSUE=Fetal brain;  
 MEDLINE=9614929;  
 Liston P., Roy N., Tamai K., Defebvre C., Baird S., Chertton-Horvat G., RA Farshani R., McLean M., Ikeda J., Mackenzie A., Korneiluk R.G.; RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes"; Nature 379:349-353(1996).

RN [2] SEQUENCE FROM N.A.  
 RP TISSUE=Fetal heart;  
 RC MEDLINE=96256286; PubMed=8564366;  
 RA Ductett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L., RA Gilfillan M.C., Shieh H., Hardwick J.M., Thompson C.B.; RT "A conserved family of cellular genes related to the baculovirus iap gene and encoding apoptosis inhibitors.;"  
 RL EMBO J. 15:2685-2694(1996).  
 RN [3] SEQUENCE FROM N.A.  
 RA Graham D.; RT Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.  
 RP [4] FUNCTION  
 RX MEDLINE=9737359; PubMed=9230442;  
 RA Devereaux O.L., Takahashi R., Salvesen G.S., Reed J.C.; RT "X-linked IAP is a direct inhibitor of cell-death proteases."  
 CC Nature 368:303-304(1997).  
 CC -!- FUNCTION: APOPTOTIC\_SUPPRESSOR. INHIBITOR OF CASPASE-3 AND  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- TISSUE SPECIFICITY: Ubiquitous, except peripheral blood  
 CC LEUKOCYTES.  
 CC -!- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -!- SIMILARITY: CONTAINS 3 RING-TYPE ZINC FINGER.  
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CC DR EMBL; U05880; AAC50373.1;  
 DR EMBL; U32974; AAC50518.1; --.  
 DR EMBL; ALI2160L; CAB95312.1; --.  
 DR HSSP; Q13490; 1QBH.  
 DR MIM; 300079; --.  
 DR InterPro; IPR01370; BIR.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF00653; BIR; 3.  
 DR SMART; SM00238; BIR; 3.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01182; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS00118; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS00089; ZF\_RING\_2; 1.  
 KW Apoptosis; zinc-finger; Repeat; Thiol protease inhibitor.  
 FT REPEAT 26 93 BIR 1.  
 FT REPEAT 163 230 BIR 2.  
 FT ZN\_FING 450 485 RING\_TYPE.  
 FT CONFLICT 162 162 S->C (IN REF. 1).  
 FT CONFLICT 423 423 Q->P (IN REF. 2).  
 SEQUENCE 497 AA; 56664 MW; 9D394C16D45EB635 CRC64;

Query Match 5.6%; Score 407; DB 1; Length 497;  
 Best Local Similarity 30.0%; Pred. No. 5.7e-17;  
 Matches 124; Conservative 59; Mismatches 152; Indels 78; Gaps 19;

QY 60 BAKRLKTFVTVYEPYSSWQEMAAAGFYFTGVSGIQCFCCSLILFGAGLTRILED-- 116  
 Db 26 EFNRLKTFANFPSSSPVSVASTLARAGFLYTGEGDVTVCFSCH----AAVDRMKGDSAV 80

QY 117 --HHRPHDC---GFLRKD-----GIAKTDIVRN-LKR----- 148  
 Db 81 GRHRVSPNCRPFNGFYLNNSATOSTNSQIONGQYKVENYLGRSDRHFDALDRPSETHADYL 140

RESULT 15  
**BIR\_CHICK** STANDARD; PRT: 611 AA.  
**ID** BIR\_CHICK  
**AC** Q09660;  
**DT** 01-NOV-1997 (Rel. 35, Created)  
**DT** 01-Nov-1997 (Rel. 35, Last sequence update)  
**DE** inhibitor of apoptosis protein (IAP) (inhibitor of T cell apoptosis protein).  
**GN** BIRL  
**OC** Gallus gallus (Chicken).  
**OC** Euteryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
**OC** Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
**NCBI\_TAXID**=9031;  
[1]  
SEQUENCE FROM N.A.  
RC TISSUE=Spleen  
RX MEDLINE=97101112; PubMed=9945639;  
RA Digby M.R., Kimpinger W.G., York J.J., Connick T.E., Lowenthal J.W.;  
RT "ITA, a vertebrate homologue of IAP that is expressed in T lymphocytes";  
RN DNA Cell Biol. 15: 981-988(1996).  
DD -  
- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).  
- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.  
- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.  
- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF T-CELL ACTIVATION IN SPLEEN AND THYMUS.  
- SIMILARITY: BELONGS TO THE IAP FAMILY.  
- SIMILARITY: CONTAINS 3 BIR REPEATS.  
- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
  
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BIR  
HSSP; Q13490; IQSH.  
InterPro; IPR001370; BIR.  
InterPro; IPR001315; CARD.  
InterPro; IPR001841; Znf\_ring.  
PFam; PF00653; BIR; 3.  
PFam; PF00619; CARD; 1.  
PFam; PF00097; zf-C3HC4; 1.  
SMART; SM00338; BIR; 3.  
SMART; SM00114; CARD; 1.  
  
**Db** 200 CFCGGKLKLNWEEGDDPMWKEHAKWPKCEFLRSKSEELIQYSGKVDITGEHFW 256  
**Qy** 197 CFSGGGLGLNWEEGDDPMWKEHAKWPKCEFLRSKSEELIQYSGKVDITGEHFW 196  
**Db** 253 SVORELPMASAYCNDSTIFATEELRIDSEKFPLKOMPRESAVGVALAKAGLFITGKIDIVOC 316  
**Qy** 257 SVORELPMASAYCNDSTIFATEELRIDSEKFPLKOMPRESAVGVALAKAGLFITGKIDIVOC 316  
**Db** 302 HCGGJGTDWKPSEDPMWQHQHKWPGCKYLLEQKGQ-EYINNIHLHSLEECLVTTKPT 360  
**Qy** 375 ---NLEDSTAVGPTYE-TAQGEQWQMFQFAKNLNEOLRAYTASFRMISLL 422  
**Db** 361 SLTRRIDDTFONPAWQEAIRMGFS--FKDIIKKMEE-KIQISCSNYSLEV 410

DR	SMART;	SM00184;	RING,	1.
DR	PROSITE;	PS0122;	BIR_REPEAT_1;	3.
DR	PROSITE;	PS50143;	BIR_REPEAT_2;	3.
DR	PROSITE;	PS50209;	CARD_1.	
DR	PROSITE;	PS00518;	ZF_RING_1;	FALSE_NEG.
KW	Apoptosis;	ZINC_FINGER;	Repeat;	Nuclear protein.
FT	REPEAT	30	97	
FT	REPEAT	176	242	BIR_1.
FT	REPEAT	262	329	BIR_2.
FT	DOMAIN	446	536	BIR_3.
FT	ZN_FINGER	564	599	CARD_4.
SEQUENCE	611 AA;	69009	MW;	53FC0136F34EBDDD CRC64
				RING-TYPE.

Query	Match	Score	DB 1:	Length	611;
Best Local Similarity	22.9%	Pred. No.	1e-15	Mismatches	142;
Matches	207;	Indels	184;	Gaps	21;
Qy	60 EAKRLKTFTYEPVSSWPPQEMAAGYFTGKWSQICQFCFCSLTLFGAGSLTRPLIEDHKR	119	Db	30 ELYRMSTESTEPVNPVPSERLLARAGAYTGTQVQDKVCFSCGLVLVDNWRQGDNAMEHKHQ	89
Qy	120 FHPDCGEL-----		Db	90 VYPSCSFVQNMNLNNLGSLSAFLSPVNLSPSLRSTLSPSPEQVGFSGCSFSFP	149
Qy	135 -----AKYDIFVKNIKSRLRGKMKYQEBEARLASFRNRPWYVOGISPVCILSEAGVP	188	Db	150 RDPVTTRAED-----SHURSKIQNPSM-----STEEARLTSHAWP--LMC1WPAAVAKAGLD	203
Qy	189 TGQDTWVOCFSCGGCLGNWESCDPPWKEHKKWFPCPEFRSKSSEETTOYI-QSYKGFD	248	Db	204 LSFADKVACVNGCYKULSNWEKDNAMESRHRHFPNCPVEN-----	244
Qy	249 IRGEHFVNSWORELPMASACVNDISFAVEELRSDFKMPWPRSAVGIAALKAGLFYTG	308	Db	245 -----LMRDQP--SPNVSNVTMQTHEARVKTETIMPTRIPVPOEQADAGFYYVG	292
Qy	309 IKDIVOCFSOGCGLEKWWEDPDRDPUHDTCFPCPNCPLONMKSSAEVTPDLSR-----G	362	Db	293 RNDVWCFCCDGGLKWCESDDPWPTEHAWWPCEYLIRVK-GGERVSQVORPHILLN	351
Qy	363 ELCELLETTEBSNLEDLSIATVGPVPEMAQEGAMOFQENKLNEQLRAAYTSASF-----	416	Db	352 SSC-----TSDKPVDEN--MDP11-HFEPGESP-SEDAIMNTPVVKAJLEMGSSRLIK	403
Qy	417 -----RIMSLDUDISSLAT-----		Db	404 QTVOISKILATEENYKTDNLVSELLTADEKREEEKEQRQFLEVASDSDLSLIRKN-----	450
Qy	451 EPLVLPVEVFGNLNSVMCPEGAEAGSGK-----		Db	458 ---RMLALFORLTSVPLTIGLSLASKVITELEHDVIKQTQTPSOARELTDIVKGNA	457
Qy	486 LWASGCCPPLNRQOLVFLSLSSTR-----PDEGLASICDOLPK--EGSVTMCMRNI	538	Db	514 ASTFRNC--LKDPDPVLYKDLFEVEKSMKVYPTEDVSGLPMWEQRLRLOBERTCKVCMDC	571
Qy	539 IQLQNOVLFLLDDYKEIC	557	Db	572 V-----SIVFIRCPGHLWVC	585

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## OM protein - protein search, using SW model

Run on: September 30, 2002, 15:01:49 ; Search time 31.33 Seconds

(without alignments) 4303.011 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 7308

Sequence: 1 MATOOKASDERISOFDHNLIL...SKYNTILQKWLPPSPRIQK 1403

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PTR\_7.1.\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	6373.5	87.2	A55478	neuronal apoptosis inhibitory protein - human
2	4919	67.3	T42628	neuronal apoptosis
3	462	6.3	S68450	neuronal apoptosis
4	431.5	5.9	S68449	apoptosis inhibitor
5	407	5.6	S69544	apoptosis inhibitor
6	345.5	4.7	S69545	apoptosis inhibitor
7	332	4.5	S68452	apoptosis inhibitor
8	326	4.5	JC5964	apoptosis inhibitor
9	303.5	4.2	A45679	apoptosis inhibitor
10	293.5	4.0	T10304	apoptosis inhibitor
11	293.5	4.0	A53989	apoptosis inhibitor
12	242.5	3.3	JC7568	kidney inhibitor
13	241	3.3	H84513	inhibitor o
14	198	2.7	T17255	probable disease r
15	194.5	2.7	T14523	hypothetical prote
16	192	2.6	S48264	cut17 protein - fi
17	181	2.5	G85188	protein kinase VPS
18	180.5	2.5	C85189	disease resistance
19	178.5	2.4	T31911	hypothetical prote
20	178.5	2.4	B85189	disease resistance
21	177	2.4	H71436	hypothetical prote
22	177	2.4	T18542	flax rust resistant
23	177	2.4	D85188	disease resistance
24	175.5	2.4	T10310	disease resistance
25	175	2.4	E82909	hypothetical prote
26	175	2.4	T06609	disease resistance
27	175	2.4	D71437	probable resistance
28	168.5	2.3	T06269	root knot nematode
29	168	2.3	T41772	IAP1 orf27 - Bomby

RESULT	1
A55478	neuronal apoptosis inhibitory protein - human
N;Alternate names:	NAIP
C;Species:	Homo sapiens (man)
C;Date:	05-Jan-1995 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
C;Accession:	A55478
R;Roy, N.; Matadevan, M.S.; McLean, M.; Shutler, G.; Yarachi, Z.; Farahani, R.; Baird, d, T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneiluk, R.G.; MacKenzie, A.	
Cell 80; 167-178; 1995	
A;Title:	The gene for neuronal apoptosis inhibitory protein is partially deleted in 1
A;Reference number:	A55478; MUID:95112344
A;Accession:	A55478
A;Molecule type:	mRNA
A;Residues:	1-1232 <ROY>
A;Cross-references:	GB:019251
C;Genetics:	
A;Gene:	GDB:SMA6; SMA
A;Cross-references:	GDB:120378; OMIM:600354; OMIM:253300
A;Map position:	5q12.2-5q13
A;Keywords:	apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane P
F;94-110/Domain:	transmembrane #status predicted <TMH1>
F;470-477/Region:	nucleotide-binding motif A (P-loop)
F;476/Binding site:	AT (Lys) status predicted <TMH2>
F;618-632/823,923,1035/Binding site:	carbohydrate (Asn) (covalent) #status predicted
Query Match	87.2%; Score 6373.5; DB 2; Length 1232;
Best Local Similarity	95.9%; Pred. No. 0;
Matches	1229; Conservative 1; Mismatches 1; Indels 51; Gaps 1;
QY	1 MATOOKASDERISOFDHNLILPELSALLGDAVOLAKELEREEDEKERAKMQGKNSQMSE 60
Db	1 MATOOKASDERISOFDHNLILPELSALLGDAVOLAKELEREEDEKERAKMQGKNSQMSE 60
QY	61 AKRILKTFTVYEPSSWIPQEMAAAGFYFGVKSGIQCFCSSLILFGAGITRLPIEDHFR 120
Db	61 AKRILKTFTVYEPSSWIPQEMAAAGFYFGVKSGIQCRCSSLILFGAGITRLPIEDHFR 120
QY	121 HDCCFLINKDVGNTAKYDTRVKNUKSRJRGKMYOREEARLASFRNWPFFYQGISCV 180
Db	121 HDCCFLINKDVGNTAKYDTRVKNUKSRJRGKMYOREEARLASFRNWPFFYQGISCV 180
QY	181 LSEAGFVFPTKQDTWOCFCGGCLGNWECDDPKEHAWPKCEFLRSKSSEBITOYI 240
Db	181 LSEAGFVFPTKQDTWOCFCGGCLGNWECDDPKEHAWPKCEFLRSKSSEBITOYI 240
QY	241 QSYKGFDVTGEHEVNSWORELPMASACNDSTFAVEYLRLSFKDPRSEAVGVALA 300
Db	241 QSYKGFDVTGEHEVNSWORELPMASACNDSTFAVEYLRLSFKDPRSEAVGVALA 300

QY	301 KAGLFYTGKIDVOCFSGGCLERKWQEGDDPLDUDHTRCFPPNCPLQFLQNMKSSEAVTPDQS	C: Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
Db	301 KAGLFYTGKIDVOCFSGGCLERKWQEGDDPLDUDHTRCFPPNCPLQFLQNMKSSEAVTPDQS	C: Accession: T42628 R: Yarachi, Z.; Diez, E.; Gros, P.; Mackenzie, A.
QY	361 RGECELETTSESNLDSIAVGPVPEMAQGEAQWFOEAKNLNBRLAYTAERIMS	Mamm. Genome 10, 761-763, 1999
Db	361 RGECELETTSESNLDSIAVGPVPEMAQGEAQWFOEAKNLNBRLAYTAERIMS	A; Title: CONA cloning and the 5' genomic organization of Naip2, a candidate gene for m
QY	421 LIUDISDLATHLLGCDLSASKHSKPSVQEPVLPEVGNCNSVMCVEGEAGSGKWL	A; Reference number: Z22179; MUID:99315342
Db	421 LIUDISDLATHLLGCDLSASKHSKPSVQEPVLPEVGNCNSVMCVEGEAGSGKWL	A; Accession: T42628 A; Status: preliminary; translated from GB/EMBL/DDJB
QY	481 KRIAFWASGCCPLNRFOLVYUSSLSPRDECILASITCDOLEKEGSVTEMCRNIQ	A; Molecular type: mRNA
Db	481 KRIAFWASGCCPLNRFOLVYUSSLSPRDECILASITCDOLEKEGSVTEMCRNIQ	A; Residues: 1-1447 <YAR>
QY	541 OLKNQVFLFDYKRCSIPQVIGKLQIKNHRSRTCLIAVTNRDIRYLETILEK	A; Cross-references: EMBL:AF102871; MHD:93860229; PIDN:AC73002.1
Db	541 OLKNQVFLFDYKRCSIPQVIGKLQIKNHRSRTCLIAVTNRDIRYLETILEK	C; Genetics: EMBL:AF102871
QY	601 AFPYNTVQILRKLFSHNTRIKFMYFGKNSLOQIOTPLFVAICAHWFQYPFDPS	C; Gene: Naip2
Db	601 AFPYNTVQILRKLFSHNTRIKFMYFGKNSLOQIOTPLFVAICAHWFQYPFDPS	Best Local Similarity 65.4%; Score 4919; DB 2; Length 1447; Matches 946; Conservative 180; Pred. No. 5e-301; Gaps 2; Mismatches 277; Indels 44;
QY	661 FDDAVAFEVSKYMERLURKATEILKATVSSGELALKGFSCFEFNDDDLASAGVD	Db 1 MATOQKASDERISOQDFINHLPLBSALIGDIAVOLAKEEERAKKQKGNSQMRE 60
Db	661 FDDAVAFEVSKYMERLURKATEILKATVSSGELALKGFSCFEFNDDDLASAGVD	Db 1 MAQGEAVEICEFDDDLSELSTLRLVALSVLKRCBEDHKTRMENKGNSQMRE 60
QY	721 EDLTMCUMSKETPAQRKPPYRFLSPAOFELAGMRLEILDSDROHQDGLGHLKQINS	QY 61 AKRLKTFYVYESSWPMQEAAGRYFTGKSGJQCFCCLSLIFGAGLTRLPIEDHFR 120
Db	721 EDLTMCUMSKETPAQRKPPYRFLSPAOFELAGMRLEILDSDROHQDGLGHLKQINS	Db 61 AKRLKTFYVYKPRSRNTPQEMAAGFYHTGKYLQVQCCRCCSLLFSTRLRKUPJENKKL 120
QY	781 PMTYSAYNNFLNYVSSLPSKTAGPKIVSHLHLVDNRESLENISENDYKHOPEISLQ	QY 121 HDGCFLNLUKVNGNTAKYDRVKNUKSRJRGKMRYQEERAKLASFRNWPFYVOGTSPCV 180
Db	781 PMTYSAYNNFLNYVSSLPSKTAGPKIVSHLHLVDNRESLENISENDYKHOPEISLQ	Db 121 RPECEFLGKDGKVNIGTKYDTRVKSPKEMRKYHREEARLESFDMPYAHGSPV 180
QY	841 MQLRGLWQCPQAVFSMVEBHLVLAALKTAYQNTVACSPVQLQFLQGRITLGALNL	QY 181 LSEAGFVFTQKDTVOCSFGGCGCJGNWEEGDDPKHEAKWPKCEFLRSKSEETOYI 240
Db	841 MQLRGLWQCPQAVFSMVEBHLVLAALKTAYQNTVACSPVQLQFLQGRITLGALNL	Db 181 LSAAGFVFTQKDTVOCSFGGCGCJGNWEEGDDPKHEAKWPKCEFLRSKSEETOYI 240
QY	901 QYFDHPESLSSLRSIHFSIRGNKTSRAPHESLTCEDKSOVPTIDQYDASAEPNNEW	QY 241 OSYKGVFDITGEHVNWSQWREMASYCNISAYEELRUDSFKDPWPSRASVYALA 300
Db	901 QYFDHPESLSSLRSIHFSIRGNKTSRAPHESLTCEDKSOVPTIDQYDASAEPNNEW	Db 241 OSYKGVFDITGEHVNWSQWREMASYCNISAYEELRUDSFKDPWPSRASVYALA 300
QY	961 ERNLAEKDVKSYMDMQRASDLSGYWKLSPKQYKIPCLEWDYNDIWVGQDMLEI	Db 301 KAGLFYTGKIDVOCFSGGCLERKWQEGDDPLDUDHTRCFPPNCPLQFLQNMKSSEAVTPDQS 360
Db	961 ERNLAEKDVKSYMDMQRASDLSGYWKLSPKQYKIPCLEWDYNDIWVGQDMLEI	Db 361 RGECELETTSESNLDSIAV----- 382
QY	1021 MTVFSASQRIELHLNHSGFISIRPALELSKAVKCSKELSAECAELLTLPSLE	Db 361 HCAPEAMETTSSENHDAAVHSTWDVSEAOBLEPASLVSVCRLRDQHSEADORG 420
Db	1021 MTVFSASQRIELHLNHSGFISIRPALELSKAVKCSKELSAECAELLTLPSLE	QY 383 ---GPV-----
QY	1081 SLEYSGTQOSODQIPNLDKFLKLKELSDLEGINTNVFSTIPEEPNFHMEKLIQITSA	Db 421 CASSGTYLPSTDGQDSEAOQWIAEANLSEQDLLTLPSE 1080
Db	1081 SLEYSGTQOSODQIPNLDKFLKLKELSDLEGINTNVFSTIPEEPNFHMEKLIQITSA	QY 437 DLSIASKHISPVQEPVLPLRPEVGMLNSTNCVEGEAGSKTLLKKAFLWASGCCPLN 496
QY	1141 EVPSKUWLTIONSPNLHVFLCKNRFSDPGSMMPLVSKKLETEIKFSDSFFQAVPEVA	Db 481 DVSITSKHISPVQDSLTIPFVEFSNLNSMCVEEAGSKTLLKKAFLWASGCCPLN 540
Db	1141 EVPSKUWLTIONSPNLHVFLCKNRFSDPGSMMPLVSKKLETEIKFSDSFFQAVPEVA	QY 497 RQLPVLPSLSTRDEGLASTCDOLEKEGSVTEMCRNIQQLKNQVFLDLYKEI 556
QY	1201 SUPNFETSLKILNLEQQPDPBETSEKFAYTGLSISNLSLEBILPTGDIYVRVAKLITOCQ	Db 541 RQLPVLPSLSTRDEGLASTCDOLEKEGSVTEMCRNIQQLKNQVFLDLYKEI 556
Db	1150 SUPNFETSLKILNLEQQPDPBETSEKFAYTGLSISNLSLEBILPTGDIYVRVAKLITOCQ	QY 557 CSIPQVIGKLUKNHSLRCLLAVTRHARDIRRYLETIEKAFPFYNTVILKLF 616
QY	1261 QLHCRLVLSPEFKTLNDSDVEI 1282	Db 601 ASLPOALHPLTILKWLRSRCLLAVTRHARDIRRYLETIEKAFPFYNTVILKLF 616
Db	1210 QLHCRLVLSPEFKTLNDSDVEI 1231	QY 677 RNKTAETLKAIVNSCCEALAKGFSCCEFNDDLAEGYDDEDLTLMSKFTAQRL 736
RESULT	2	Db 721 KHKGAAPLQATVSSCGOLALTGLPSSCFFNSDNLAEQVDEDEELTCLMSKFTAQRL 780
T42628	neuronal apoptosis inhibitory protein 2 - mouse	QY 737 RPYRFLSPAFQFLAGMLTLELLSDROHQDGLYHJKQINSPMMYSAVINFLIVS 796
C; species: Mus musculus (house mouse)	"	



Db	35 TYSSTEPAGPVPSERSLARAGFVYTGVNDKVKFCGGMLDNWKRQDSPTTEKKLYPSCR	94
Oy	125 FLLN-KDVGNCI-----	
Db	95 FVOSLNISVNVNLNEATSQPTFPSSVTHSTHSLPGTENSYFRGGSYNSPSNPNSRANQE	154
Oy	151 GGMR----YQEEARLARSFRMNPFFYQOGISPCVSEAGFVFTGKODTQCFSCGGCL	150
Db	155 SALMRSYSPCPMMNNEMARLTFTQWP---LTFLSPTDLARAGFVYIGFDRVACFAGGKL	204
Oy	205 GWEEGDDPPKEHAKWPKPEFLSKKSSETIQTQYQSYKGFVDITGEHFVNWSORELP	212
Db	213 SNWERPDNAESEHLRHFKCPFIENQ-LQDTTSRTVS-----	264
Oy	265 MASAVCNDSTFAYEELRUDSFKEKOMPRESAVGAALAKAGLYTGKDIVQCFSCGGCL	1
Db	252 MOT-----HAARKTFFPWNSSVLPNEOLASAGVYVVGNSDDVFCFCGGGLRC	301
Oy	325 WOEGDPPLDDHTCFPNCPFLQNMKSSAETPDLSRGCELCLETTSES-----	375
Db	302 WESGDDPPWQHAKWPKPECYLIRIKQEFPRQVQSYPHILEQOLISTSDSPIDENAASSI	324
Oy	362 IHLEPGEDHSDEAIMMTPIV----NAVENFGSRRSLVKDQVORILAGENY-----LV	413
Db	426 SOLATBHLGCDLSTASKHISPKVQEPVLPEVFGNLNSVMCGVEGRAGSGTKVLUKKIAF	450
Oy	486 LHASGCCPLLNRFOLVFYLSLSSTRPDEGL-ASITCQ-----	449
Db	450 -----NRMALFOHLLTCVPIVPLSLLTAGILNEQEHVWIKOTQSLQAREBLDTI	526
Oy	527 --EGSYTEMCMRMNTIQLK--NQVLEFLDK----ETCSPIROVIGLQKHLSTC	576
Db	500 LVKGNAIAAVFVRSLOEAEEVLYEHLFVQDQPKYIPTEDVSDLP--VERQLRRLPEERTC	499
<b>RESULT 5</b>		
	659344 apoptosis inhibitor IAP homolog - human	
C;Species	Homo sapiens (man)	
C;Accession	06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000	
R;Duckett, C. S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C.;Title: A conserved family of cellular genes related to the baculovirus iap gene and er		
A;Accession	S69544; MUID:9256286	
A;Status	preliminary; nucleic acid sequence not shown	
A;Molecule type	mRNA	
A;Residues	1-497 <DUC>	
A;Cross-references	EMBL:U32373; NID:91019116; PIDN: AAC47155.1; PID:9101917	
C;Genetics	I10	
C;Superfamily	apoptosis inhibitor IAP homolog; RING finger homology <RRN>	
F;446-490/Domain	RING finger homology	
<b>Query Match</b>		
Best Local Similarity	4.7%	Score 345.5; DB 2; Length 497;
Matches	114; Conservative	Pred. No. 6.1e-14; Gaps 16;
A;Accession	NID:91016687; PIDN:AC50518.1; PID:91016688	
A;Title	Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP	
A;Accession	S68451	
A;Status	nucleic acid sequence not shown	
A;Molecule type	mRNA	
A;Residues	1-161; C, 163-422; O, 424-497 <LIIS>	
A;Cross-references	EMBL:U45880; NID:91184319; PIDN: AAC50373.1; PID:91184320	
A;Gene	I1P	
C;Function	apoptotic suppressor	
C;Superfamily	apoptosis inhibitor IAP homolog; RING finger homology	
C;Keywords	apoptosis; zinc finger	
F;446-490/Domain	RING finger homology <RRN>	
<b>Query Match</b>		
Best Local Similarity	4.7%	Score 345.5; DB 2; Length 497;
Matches	114; Conservative	Pred. No. 6.1e-14; Gaps 16;
Oy	57 MRSIAKRLKTFWYEPISSWPMMAAGTYFTGVKSGIQCFCSLIL-----FGAG 108	
Db	6 MELESVRLATFGEWPLNAPVAEIDLIVANGFATGQWLEBCHCVRIDRWYXGDOVAG	65
Oy	109 LTRPLTDHKRPHDGGFLNKD-VGNTAKYDITRKVNLKSRLLRGKMYQREAA-----	
Db	66 -----HRSSPKCISMVLAQNHCGNVP-----RSQESDNNEGNSVDSPECSCPDLI	161
Oy	162 ---RLASFRMPPFWQGISPVCVSEAGFVFTCKQDVOCTSCGGCLGNWEEGDPWKEH	217
Db	112 LEANRUVFKDW-----NPNTPOALAKGFFYLRLDHWKCVNGVIAKWEKNNAFESH	217
Oy	218 AKWFCK-----EFLRSKSSSEETQYQSYKGFVDITGEHFVNWSORELPMSA	169
Db	170 KRFPPQCPVQMGPLIEFATGKNUDE-----LGIQPT-----LPURPK 208	268
<b>Query Match</b>		
5.6%; Score 407; DB 2; Length 497;		

Best Local Similarity 30.0%; Pred. No. 8.2e-18; Matches 124; Conservative 59; Mismatches 152; Indels 78; Gaps 19;

Db 60 EAKLKTPTVYESSIIPOMRAAGFVFGVUKSICQCCSULIFGQALTRAPIED-- 116

Db 26 EFNRLKTFANFPSPGSPVASTLARAGFLTGEGITVRCFSH----AAVDRWQGDSAV 80

Oy 117 --HKRFHPDC---GRULLNKV---GNTAKYDIRVN-LKSR----- 148

Db 81 GHRRKTPSPNCRPFINGSYLENSTATOSTNSQYQKVNWLSDRHDALDRPSETHADYL 140

Oy 149 LRGKMK-----RYQEEARLASFPRMNPFFYQGISMCPVULSEAGFVFTGQDWTQ 196

Db 141 LRTQWVDSITIYPRNPAMPSYEARUKSFQWNPDYAH-LTRELASAGLYYIGDQYQ 199

Oy 197 CFSCGCCLNLWECDDPDKPHAKWPKPEFLSKKSEETIQYQSYKGFVDITGEHVN 256

Db 200 CFCCGGKLNLWECDDPDKPHAKWPKPEFLSKKSEETIQYQSYKGFVDITGEHVN 256

Oy 257 SWYORELPMASACNDSTFAYEELRUDSFKEKOMPRESAVGAALAKAGLYTGKDIVQCF 316

Db 253 S---TNLRP----NPSMADY-EARIFTFVW-TYSVNRQELARAGYIALEGDKYKCF 301

Oy 317 SCGCGCLNLWECDDPDKPHAKWPKPEFLSKKSEETIQYQSYKGFVDITGEHVN 251

Db 302 HCGGLTDWKPSDPEWQHAKWPKCQVYQLEQKGQ-EYINNTLTHSLBECLVTRTEKP 352

Oy 375 ---NLEDSIAVGPVPE-MAQGEAQWQEQAKUNLNEOARAATSASFRHMSL 422

Db 361 SLTRRIDDTTFTONPMPVQEARMGS---FMDIKRIMEE-KIQJSGSNVSKLEV 410





A;Residues: 1-1215 <STC>  
A;Cross-references: GB:AE002093; NID:9659871; PIDN:AAD25848.2; GSPDB:GN00139  
C;Genetics:  
A;Gene: Atg14080  
A;Map position: 2

Query Match 3.3%; Score 241; DB 2; Length 1215;  
Best Local Similarity 19.8%; Pred. No. 8.9e-07;  
Matches 226; Conservative 165; Mismatches 383; Indels 370; Gaps 52;

QY 368 LET'SESENLEDSTAVGPTVPEMAG-----EAOW----- 396  
Db 84 IDTFIDNNIERSKISIGPELLEIAVRGSKIAVVLISKDYASSWCLNELYBIMKCRMLDOT 143  
QY 397 ---FQE-----AKUNNEQLRAAYSASFRHMSLDISSLATDHLGCDS 439  
Db 144 VMTLFYEVDPTDVKKTGDFGKFKKTGKTLNDSSWEAKVATSG----- 203  
QY 440 IA-----SKHISKPVQEPLVPLPEVFG-----NLNSVMCBE-----GEAGSG 475  
Db 204 AAMEKISTDISKNKLANNSTPLRFDGLVGMGAMEMKELELLCIDSCEVRMIGIWGPPGIG 263  
QY 476 KTVLKKIAFLWASGCCPILNRCOLVFYI-----SLSSTRDEGLASICOLLER-- 536  
Db 264 KTTIVR--FLYHQ---LSSRFELSMITEMKTMHTILASSDDYSAKULIQQFLSKIL 316  
QY 527 EGSYTEMCMRNITQOQ-LKNQVIFLDDYKEICSIPOVIGKLQKHNHSRTCTLIJAVRTN 584  
Db 317 DHKOTIEPHILQYERLYKKVWDLDD-----VDSYDQALAKETWFGPES 365  
QY 585 RADIRTRYLETIEIKAFPFYNTVCILRKLFSHNTRKRFMY-FGKNOQSKIOKTP- 642  
Db 366 -----RLITTDQRKLLKAHRINNIYKVLDPNSDALQIFCMYAFG-----OKPY 411  
QY 643 --LFEVAATCAHWF--QYRFPSPFDDAVYFKSYMRLSLRKNAKATEI-LKATVSSCGELA 636  
Db 412 DGFYKLARKVTWLVGNFPL---GLRVVGYSYFREMS-KOEWKEKEIPRLRARIQDGKIESV 465  
QY 697 LKGKFSCCEFNDDLAEGVDEDIDLCLMSMSFTAQLRPVTFRLSAFAQOFLAGMRL 756  
Db 466 LK-----FSPVACL-----DEKDLEHIACTCNHESIEKLEDPLGKTF---- 504  
QY 757 IELLSDSDRQEHODIGLYHLQKINSPPMMTVSAYNNFLNVYSSLPSTKAGPKIV----- 808  
Db 505 --LDAIQRFH-----VIAEKLISINSNFENVEMDSL-AQISKEIVKQSVRPP 549  
QY 809 SHLHLVDRKESLNITSENDYLIKHOPEISLQMQLLRG--LWQICPOAYFSMSEHLLYL 866  
Db 550 GOROFLVDRDISEVLA--DDTAGGRSVIGIYLQDHLHRNDDVFNISEKAREGM--SNLOFL 605  
QY 867 ALKPAQYOSNTVACASPFV-QFLQGRTLTGALNQYFFDHPEISLRSIHFPIRGNTS 926  
Db 606 RVKNGNGLNPATVOLPHCYTIS-----RKURLLDQMP----- 641  
QY 927 PRAHESVLETCFDKSQVNPTIDQDAYSAREP---MNEMERNAEKEDNVKSMIDMORA 981  
Db 642 -----TCF-----PSKFNPFLVELNMGSKFLKWEIQPLURNLR-- 678  
QY 982 SPDLSITGYWKLSPKQYKPKCLEVNDIVGQDMLEILMTVFAASORIELHNNHSGFI 1041  
Db 679 -----MDLFSKNLKELPDLSATNLEVNLNGCSSLV 711  
QY 1042 ESRPAPALESKASYTKCSISKLSEAAEGELLILPLSLESLEYSGTISQDQIFPNLDFK 1101  
Db 712 E-----LPPSIGNATK---LJKLSELGCS---LLELPS---SIGNAINQITPSHCEML 758  
QY 1102 L-----CLKEKSVLEGINVNVSYTPEEPFNPHMEL-LIQISAEYPSKVLK 1150  
Db 759 VELPSSIGNATNLKELDUSCSSL---KELPSIGNCTNLKLUHICSS---LKELEPSS 812  
QY 1151 IQNSPNLHVFHLKC---NFFSDGSLMMF---LVSKKLITIKFSDSFFQAVPFVAS 1201

RESULT 14

T17255 hypothetical protein DKFZp58601822.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 15-Oct-1998 \*sequence\_revision 15-Oct-1999 \*text\_change 15-Oct-1999

R;Koehrer, K.; Beyer, A.; Meves, H.W.; Gassenhuber, J.; Wleemann, S.

submitted to the Protein Sequence Database, September 1999

A;Reference number: Z18722

A;Accession: T17255

A;Status: Preliminary

A;Molecule type: mRNA

A;Cross-references: EMBL:All117470

A;Experimental source: adult uterus; clone DKFZp58601822

C;Genetics:

A;Note: DKFZp58601822.1

Query Match 2.7%; Score 198; DB 2; Length 1192;  
Best Local Similarity 20.8%; Pred. No. 0.00044; Mismatches 282; Indels 212; Gaps 34;

Matches 158; Conservative 108; Mismatches 282; Indels 212; Gaps 34;

QY 450 QEPVY-----LPEVFG-NLNS---VNCVEGEAGSCKTUVLKKIAFLW 487  
Db 11 QDPLVVKRSRNPDVYEENRGHHLTEIRDQFLGHDQEPRTVLOGAGIGRSTLARQKEW 70  
QY 488 ASGCCPPLNPKPOLYFYLSLSSTRDEGLASICOLLENEVGSYTEMCMRNIIQOLKNQL 547  
Db 71 GRGQL-YGDRFQHVYFVFSCRELAQSK--WVSLAELIGKQGTATPAPTRQILSR-PRFL 125  
QY 548 FLLDDY-----KEIC--SIPQ---VIGKLQKHNHSRTCTLIJAVRNARDI 589  
Db 126 FILGDVDEPQWVQLOEPSSBLCHWSQPOLADALLGSLIGKTILEPEASFLLTARTALQNL 185  
QY 590 RRYLETI-LEIAKPFYVNCILRKLFSHNTRKRFVYFGNNSQSKIOKTPFLWA 647  
Db 186 IPSLQCARWVNLQFSESSRKEYPYRFDRQIAFRFL-VKSNEKELWALCVPWVSHL 244  
QY 648 ICANHFOYQFDPSPFDDAVYFKSYMRLSLRKNAK-----AELKATVSSCGE 694  
Db 245 ACTCLMQ-----MKRREKLITJSKTTLCHYLAQOLQROPLQGQLRDXCS 292  
QY 695 LALKGFFSCCFEFNDDLAEGVDEDIDLCLMSMSFTAQLRPVTFRLSAFAQOFLAGM 754  
Db 293 LAAGEIWKKTFLSPDDLRKHGLDGA11STFLKMGILQHPIPLSYSFTHLCFOEFFAM 352  
QY 755 RLIEUDSDRQEHODIGLYHLQKINSPPMMTVSAYNNFLNVYSSLPSTKAGPKIVSHLHL 814  
Db 353 SYVLEDEKRGKHSNC-TIDLER-----TLEAYG----IHGL---PGASTTRFLGG 396  
QY 815 V-DNKESLEN-----SENDYLIKQPIPLSQMO---LRLQWQICQPAVFSMVSEH 862  
Db 397 LSDEGEREMENIFHCRLSOGNLQWVPSLQLLOPHSLESHLQLYETRNKTEFTQVMH 456

QY 863 L--LVALKTAQOSNTVAACGSPF---VLOQFLQGRLTGALNQYFFDHPESLILRS 915  
 Db 457 FEEMGMGVETDMELLVCTFCIKFSRHVKKLQIEGR-----K 503  
 Qy 916 IHPFRGNKTSPPRAHFSVLTCDKSQOPTIDYSAFEPMENWRNLAE-----K 967  
 Db 504 VLF-----RWPVPTDAYWQIFLSVL-KYTRNKELDGSNL 540  
 Qy 968 EDNIVSYMDMORRA-----SPDLSTGWWKLSPROYKIPPCLEVDVNDI 1009  
 Db 541 HSAVKSLLKTLPRLPCLLETLRLAGGLTATDCKDIAFG--LRANQ-ILTEEDLSFNL 596  
 Qy 1010 DWVG-----ODMLBLIMVFSASQRIELHLMHS---- 1037  
 Db 597 TDAGAKHLCORIQRQPSCKLQLQLVSCGLTSDCCODLASVLSASPSSKELDQNNLDD 656  
 Qy 1038 -RGFISIRPALELSKASTTKCSTS--KLELSAEOE 1071  
 Db 657 GVRLLCEGLRPACKLIRLGIDQFTLSDENRQELRALEQE 696

RESULT 15

T43523 cut17 protein - fission yeast (Schizosaccharomyces pombe)  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 02-Jun-2000  
 C;Accession: T43523; T41649; T41700  
 R;Moriishi, J.; Matsusaka, T.; Yanagida, M.  
 S;Submitted to the EMBL Data Library, August 1999  
 A;Description: Fission yeast cut17 is required for chromosome segregation.  
 A;Reference number: Z22536  
 A;Accession: T43523  
 A;Status: translated from GB/EMBL/DDJB  
 A;Residues: 1-997 <WDR>  
 R;Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
 A;Reference number: Z22007  
 A;Accession: T41649  
 A;Status: translated from GB/EMBL/DDJB  
 A;Residues: 1-997 <HAR>  
 A;Cross-references: EMBL:AL031323; PIDN:BAAB3415.1  
 A;Experimental source: strain 972h; cosmic c962  
 R;Weder, H.; Buersterhoet, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
 A;Reference number: Z22010  
 A;Accession: T41700  
 A;Status: translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Cross-references: EMBL:AL121859; PIDN:CAB58376.1; GSPDB:GN00068; SPDB:SPCP31B10.10C  
 A;Genetics: cut17; SPECCH2-02C; SPDB:SPCP31B10.10C  
 A;Map position: 3L  
 A;Introns: 4/3

Query Match 2.7%; Score 194.5; DB 2; Length 997; Best Local Similarity 19.0%; Pred. No. 0.00055; Matches 232; Conservative 177; Mismatches 447; Indels 365; Gaps 60;

Qy 147 SRLRGKMRQEEEARLASF--RWMPFVYOGTSPCVLSEAGEVFT-----GKDTQV 196  
 Db 13 NRPREMNCYSK--RLDPFQKKWPRAKP--TPETLATVGFYVNPISENSEENSEEDNVT 67  
 Qy 197 CFSCGGCLGLWEECDDPWKEAHKFPKCEFLRSKKSSEEIQYISYKGFDITGEHFVN 256  
 Db 68 CYMCYKSFYDWEDEDDPKHEITHSPSCPW-----AYILSK-----N 105  
 Qy 257 SWVRELPMASAVCNDSFIAVEELRLJSFKDWPRESSAVGVAAKAGLFY--IGIKDIV 313

Db 106 NPNONPOQAALTKCRQTFVDKVWRYTNRPDYRCEPSV---MAASFVYNTADAKDA 161  
 Qy 314 OGFSCGCCLEKWKQEGDPLDHTRCFPMRFLQMKSSAENVTDLSORGELCELLPTSE 373  
 Db 162 HCLYCDINLHWEPDDPDTTEHKRRRADCFVFF-TWKDPPNSUPTKLS----FLSTSH 213  
 Qy 374 SNLEDSTIAVGPVPEMAOEAOWKQEAKNLNEOLRAYTSASFRHMSLSDISDAATDH 433  
 Db 214 IDPEDLTEDNSILPVSPTRDST--KSHMTLN----FSPERKNNNARPLTMSLYT-- 262  
 Qy 434 LGCDLSIASKHISKPVQ-----EPLV-----PEYFGNLISVMYVEGEAG 473  
 Db 263 -----NTSREKSDQPTRAQSPNPKSPKSKPAFKPKVPIFSDDEDD 317  
 Qy 474 SGKTVLKKKIAFLWASGCC-----PILL----NRQOLVYLSSSTRDE 513  
 Db 318 DDUTA----SQPFSGKICNDMSMQAVKNNFEEIPKEDKDNE--HLVSPATSHT 369  
 Qy 514 GLASICDCOLLKREGSYTMCM--RNQQLKNOVFLDDYKETCSIPQVIGLK 569  
 Db 370 TVSDITGHQSVIDESDEQNMSTPRKIEKSFEEELSVWSKESVSSVSK-----EQ 427  
 Qy 570 NHSLRTCLLIAVRTNARDRRLYLETILEKAFPFYNTVCILRKLFESHNMTRKENVF 629  
 Db 428 NTERKO--VAETPQQVKVEKEDHL-----NLQGSFTEESTK----- 463  
 Qy 630 GRNQSLQKIQKTPLEPVAACTAHWQYPFDPSSFDVAV---FKSMERLISLRNKAET 684  
 Db 464 -----OPISKP-----SPSSPDMDAVGRGRSSSSFRDKILQTNFSP--- 502  
 Qy 685 LKATVSSCGGLAKGKFSCCFERNDDLAEGYDEDEDLTWCLMSIFTAQRRLPYRFLS 744  
 Db 503 -RSTDPSFNISKRNSE--EANDE-----NDETNLKIPIPEK-----K 538  
 Qy 745 PAFBELAMRULLELDDDRHQDILYHLKQINSPPMTTSAVNNFLVYSSLPTKAG 804  
 Db 539 RKFOEVLOSKNT--LVSTEDSHEPV--KTYEDSOTAIWVSKEFDLEN----- 582  
 Qy 805 PKIVSHLHLVNDKNELENI--SENDYLYKHOPEISLQHOLRLWQICPOAYFSMVSEH 862  
 Db 583 -----KSMSEOSLQIQLSEEND---KPLIDL----- 607  
 Qy 863 LLVALKTAQOSNTVAACGSPF---VLOQFLQGRLTGALNQYFFDHPESLILRS 963  
 Db 608 IPPLAIIK--KDNLYSG---VLE--KGKSTSTSKT---FD---TSIVDPIE--- 646  
 Qy 923 NKTSPPRAHFSL-----ETCFDSQVPTID-----QDMSAF----BPMNEWR 963  
 Db 647 --KPKTEISELVPEEKRRKACIDQSQTVRSLDRGVTKTRDVSSPVSEKSENVHEAN 703  
 Qy 964 LAEKEDNVKYMMDMORRASP-DIYSTG-YWLSP---KQKIKPCLEVDVNDIDVGD 1016  
 Db 704 SGHTVMMVHSSLDQPIQVNPENELEGSLKDFDRNGNSKTYQEDDINSPLQSKR 763  
 Qy 1017 LEILMTVFSASQRI-ELHLMHNRGFISSIRPALELSKASVTKCSTSKLESA--EOELL 1073  
 Db 764 OTVEAVNTSDSLSQKEPANHELENIEKIEKL-----TEVDKVSLSARPDKOIK 814  
 Qy 1074 LTPLSLESLEVSTQSDQDIPNPLKFLCKLPSLVDLEGNTINFSVTFEEFNHMEK 1133  
 Db 815 NSRMSVQ----NGT-RSVSKNPE-----KETKVKDIDVNSKVD--ETSPGSCETSS 860  
 Qy 1134 LLIQISABYDPSKLVLKIONSP-----NLHVFLKLCNFSDFGMLMTMUSC 1180  
 Db 861 AFAKTIVREKEVSI----NLPSVRLPDBSYXHHSISFDPICQ--SSFLAPPTPK 913  
 Qy 1181 KLTETKFSDSFQAVPVFASL-----PINFISLKLNLNGQOEP-----D 1220  
 Db 914 HALPVLVEANAPPWEPIDFSSLLESPVPNVEPWNKULSEKLDWTEQWIKEMVAKAKEE 973  
 Qy 1221 EFTSEKFAVILGSLSNLEEL 1241

Tue Oct 1 09:27:21 2002

us-09-830-338-1.rpr

Page 9

Db 974 EACEEKIEWLLEGKRAEYI 994

Search completed: September 30, 2002, 15:05:37  
Job time: 228 sec

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OM protein - protein search, using sw model  
Run on: September 30, 2002, 15:03:24 ; Search time 49.94 seconds  
Title: US-09-830-338-1  
Perfect score: 7308  
Sequence: 1 MATQGRASDERISQFDHNL.....SKVLTILQKWLRFSPRIQK 1403  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPREMBL\_19:  
1: sp\_archea:/\*  
2: sp\_bacteria:/\*  
3: sp\_fungi:/\*  
4: sp\_human:/\*  
5: sp\_invertebrate:/\*  
6: sp\_mammal:/\*  
7: sp\_mhc:/\*  
8: sp\_organelle:/\*  
9: sp\_phage:/\*  
10: sp\_plant:/\*  
11: sp Rodent:/\*  
12: sp\_virus:/\*  
13: sp\_vertebrate:/\*  
14: sp\_unclassified:/\*  
15: sp\_rvirus:/\*  
16: sp\_bacteriaph:/\*  
17: sp\_archeap:/\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1894	25.9	597 11 Q9R015	09r015 mus musculus
2	486	6.7	589 11 Q9ESE8	09ese8 rattus norvegicus
3	486	6.7	589 11 Q9QZC6	09qzc6 rattus norvegicus
4	457.5	6.3	602 11 Q9ESE9	09ese9 rattus norvegicus
5	439	6.0	610 13 Q9T319	09t319 gallus gallus
6	427.5	5.8	374 11 Q921N0	0921n0 mus musculus
7	416.5	5.7	501 11 Q9EQ05	09eq05 rattus norvegicus
8	416.5	5.7	501 11 Q9EQ04	09eq04 rattus norvegicus
9	409.5	5.6	496 11 Q9ESF0	09esf0 rattus norvegicus
10	386	5.3	324 13 Q9DDN2	09ddn2 gallus gallus
11	336	4.6	498 5 Q960U3	0960u3 drosophila
12	325	4.4	87 11 Q99123	099123 mus musculus
13	323.5	4.4	195 13 Q9IA70	09ia70 gallus gallus
14	323.5	4.4	197 13 Q9IA69	09ia69 gallus gallus
15	320	4.4	87 11 Q99119	099119 mus musculus
16	316	4.3	87 11 Q99120	099120 mus musculus

Db	2 KMKKGNSQNSRSEAKRLKFETVDTFRSHTPOEMAAGFHTGYRLGVQCRCSSLILFGN 61
Qy	108 GLTRPPIEDIKREHPDCFLNLNKDVGNIAKDIRYKLNLRSRQGKMYQEEARLASFR 167
Db	62 SLRKLPYERKKLRPECEFLCKDVGNIYGDYKRPMLGGKARYHBEARLESFE 121
Qy	158 NWPPIVOGJSPCVLSEAGFVFTGKDTQVOCFSCCGCLGNMEGDDPWKEHAKWFKCFL 227
Db	122 DWRYAIGTSPRVLSAGFVFTGKDTQVOCFSCCGSLGNWEGDDFWKEHAKWPKCFL 181
Qy	228 RSKSSEETQYIQSFKGFDITGEHFHNWSWORELLMASAYCNSISAYEERLSDK 287
Db	182 QSKSSEETQYIQSFKGFDITGEHFHNWSWORELLMASAYCNSISAYEERLSDK 287
Qy	288 WPREASVGVALAKAGLFYTGKDTQVOCFSCCGCLGNMEGDDPWKEHAKWFKCFL 241
Db	242 WPOESPVGVYALVRAGEFTGKDTQVOCFSCCGCLGNMEGDDPWKEHAKWPKCFL 347
Qy	348 MKSSAEWPPDLSRGELCELLETTSEMSLEDLSAVGPVTPEMAQEAQWFOEAKNLNEQI 301
Db	302 LKSSAOVITPLQSOYALPETAETTRESNHDAAV..... 407
Qy	408 RAATSAFSRHLMSLDISSBLATDHLCGLDLSTASKHISKVQEPLVLPEVFGNLNSVMC 336
Db	337 ..... 467
Qy	468 VEGEAGSGKVYLLAKIAFLWASGCCPLNRLPQVFLSLSSTRDEGLASICDQLEKE 336
Db	337 ..... 528 GSVTBMCMRNIIQQLKNVFLQFLDDYKETCSIPVIGKLIQKHLSTCILIAVRNR 527
Db	337 ..... 588 DIRYLETILEIKAFPFYWCILRKLFSHNMTRLRKFMVYFGKNSQLOKIQKTPFLVAA 587
Qy	588 ..... 336
Db	337 ..... HSTV..... 647
Qy	648 ICAHWIYOFPDPSEPDVAVFKSYMERLSSLRNKATABILKATVSSGELALKGFSCCEF 340
Db	341 ..... 708 NDDDLAECVDEDLTMCLMSKFTAQORLRFYRFLSPAFOEQERLAGMRLIELLDSDROEH 707
Db	341 ..... 768 QDQLYLHLKQTNSPMHTVSYANNFLNYVSSLPLSTKAGPKIVSHLHLVONKESENISEN 827
Qy	828 DYLKHOPEISLQMLRGLWQCPQAIFSMVSEHLLVALKTAQOSNTVAACSPFVLFQ 887
Db	341 ..... 888 LQGRFTLTGALNHQYFDRHPESSLRLSIHPIRKNTSPRAHESVLETCDFKSQVTID 947
Qy	948 QDYASAFPMERNERNLAKEEDNVNSYMODMRRAISPOLSTGYWKLSPKQVKIPCLEVDN 340
Db	341 ..... 1008 DIDVVGODMELBILMTVFSASORTIELHLHNSRGFIESTRPALELSKASYVTKCSISLSEA 1067
Qy	1068 AEQEULIUTPSLESLEVSGTQSODOLFPNLDFKFLKELSVLEGNIINVSVIPEFPN 340
Db	341 ..... 1128 FHNHEKLUQIQAEDYDSKLVKLIONSPNHLVFLKCHPFSFGSANTMUSCKKLETEK 1127
Qy	341 ..... 123 FGTGKOPTVOCFSCCGCLGNWEGDDPWKEHAKWPKCFLRSKSSERITOYIOSYKG 381
Qy	1188 FDSDFPOAVPFVASLPLNPNTSLKILNLFGQOPDETSFEPAYLGSLSNLEPLIPTGDS 382
Db	1188 FDSDFPOAVPFVASLPLNPNTSLKILNLFGQOPDETSFEPAYLGSLSNLEPLIPTGDS 1247
Qy	1248 TYRVALTIQQOQLKRLVSEFFKTLNDSVYIAKAWISGFOKLENKLSTHKITE 1307
Db	442 IHQVAKLIVROCLQPLCYLTERHDILDDSVEIARATAQGFKLENKLSTHKITE 1307
Qy	1308 EGURNFQALDNMPNQELDISRHFTECKIACATVYKLSOCVRLPRIRLNLSWLD 501
Db	502 EGYRNFOQALDNPLNQELNICKRNPGRIVQRTTVKALQCVSRPLSLRHMWSLWD 1367
Qy	1368 ADDIALNVMKMERIPOSYLTQKWLPSPII 1401
Db	562 EEDMVKINDVYKERIPOSKRLIFWKLIVPPSPVI 595
RESULT 2	
Qy	09E8B
Id	09E8B
Ac	09E8B
Prt	PRELIMINARY;
Dt	01-MAR-2001 (TREMBLREL. 16, Created)
Dt	01-MAR-2001 (TREMBLREL. 16, Last sequence update)
De	INHIBITOR OF APOPTOSIS PROTEIN 2.
Os	Rattus norvegicus (Rat).
Oc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX
Rn	NCBI_TaxId=10116;
Rp	SEQUENCE FROM N.A.
Ra	HOLICK M., LeFebvre C.A., Hicks K., Korneluk R.G.,
Rt	Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes.
Rl	Submitted (SEP-1999) to the EMBL_GenBank/DBJ databases.
Cc	-- SIMILARITY: CONTAINS 1 KING-TYPE ZINC FINGER.
Dr	EMBL: AF182431; AAC22971.1; -
Dr	INHIBITOR OF APOPTOSIS PROTEIN 2.
Dr	HSSP: Q1390; IOBH:
Dr	InterPro: IPR01370; BIR.
Dr	InterPro: IPR01315; CARD.
Dr	InterPro: IPR01841; Znf_fing.
Dr	PFam: PF00653; BIR; 3.
Dr	PFam: PF00619; CARD; 1.
Dr	SMART: SN00238; BIR; 3.
Dr	SMART: SM00114; CARD; 1.
Dr	SMART: SM00184; CARD; 1.
Dr	PROSITE: PS0128; BIR_REPEAT_1; 1.
Dr	PROSITE: PS0113; BIR_REPEAT_2; 3.
Kw	Zinc-finger; CARD; 1.
Sq	SEQUENCE 589 AA: 66750 MW: B4F7089BD7CD285B CRC64;
Query Match	
Best Local Similarity 6.7%; Score 486; DB 11; Length 589;	
Matches 154; Conservative 75; MisMatches 186; Indels 138; Gaps 23;	
Qy	41 EERERAKMOKGNSQNSRSEAKRLKFETVDTFRSHTPOEMAAGFHTGYRLGVQCRCSSLILFGN 97
Db	12 KERKE - KMKIDFSC-----LYRMASTYSAPPGRGVPSERSLARAGYYTCVNDKVC 98
Qy	98 FCCSLILFGAGLTFRLPIEDHKRHRPHDGF--LINKDVGAIAKIDDIRVN----- 62
Db	63 FCCGLMLDNWKQGBSPTEKHROFYPCSFVQTLGGIOLA 144
Qy	145 -----LKS-----LRGKMR--QEEARLASFRNWPFVQGSPCVLSEAG 122
Db	123 GGTRSSLSPNPLNSRAVEDFSLIRMPCSTAMSTEAPLFSWMP--LSLSPLAELAKAG 180
Qy	186 FVTGKOPTVOCFSCCGCLGNWEGDDPWKEHAKWPKCFLRSKSSERITOYIOSYKG 245

Db	181	FYIITGPDDRYACFACGGKLSNWEPPNDPSEERRHHPHCPLFLENTSETORFS-----	232
Qy	246	FVDITGEHFVNSWORELPMASAYCNDSTFAYEELRDSLKDWPRESAVGAALAKAGLF	305
Db	233	-----VSNLSMOT-----HSARMSTFLYWPSSVLVPEOELASAGFY	268
Qy	305	YTGKDIVOCFSCGGCLEWQEGDPLDDHTRCFPNCPCPLQNMKSSAEWPDLQR-GEL	364
Db	269	YVDHNDVCFCCPGLRWEPGDPWIKHAWPCKEFLIRMGQ-EVDEIQARYPHL	327
Qy	365	CELLETTSSNLEDIAVGPPIVEMAQGEHOWEAKNIEOLRAYTASFRHMSLDI	424
Db	328	LEQLISTSDTSEEEN-ADPPVWHGPGE-NW-EDAVMTPTVKA-----	369
Qy	425	SSDLATDHLLGCDSIASHKISKPVQEPLVLPVEFGNLNSVMCV-----EGENG	473
Db	370	----ALD--MGFSRSILVRQIVQVORI--LATGENRTVSDIVSALLNAEDERREKEKERQ	420
Qy	474	SGKTVLKKIAFLWASGCCPPLNRQVFLVYLISSTRPDEGLASICDQOLKEGSYSTEM	533
Db	421	SEET-----ASGDSLIRKNRMALFOQLTCVIP-----ILDLL-BASVLT	461
Qy	534	CMRNITIQLKNOV 546	
Db	462	EEDHDIRQ-KTOI 473	
RESULT	3		
09QZC6		PRELIMINARY; PRT; 589 AA.	
ID	09QZC6		
AC	09QZC6;		
DT	01-MAY-2000 ("TREMBLel. 13, Created)		
DT	01-MAY-2000 ("TREMBLel. 13, last sequence update")		
DE	INHIBITOR OF APOPTOSIS PROTEIN 2.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.		
OX	NCBL-TAXID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-KIDNEY		
RA	Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.,		
RT	"Cloning of cDNA for rat inhibitor of apoptosis protein 2.";		
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.		
DR	EMBL; AF19020; AAF04585.1; -.		
DR	HSSP; Q13490; 10BH.		
DR	InterPro; IPR001370; BIR.		
DR	InterPro; IPR001315; CARD.		
DR	InterPro; IPR00141; Znf_finger.		
DR	Pfam; PF00653; BIR; 3.		
DR	Pfam; PF00619; CARD; 1.		
DR	Pfam; PF00097; zf-C3HC4; 1.		
DR	SMART; SM00238; BIR; 3.		
DR	SMART; SM00184; CARD; 1.		
DR	SMART; SM00184; RING; 1.		
DR	SMART; SM00184; RING; 1.		
DR	PROSITE; PS01182; BIR_REPEAT_1; 3.		
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.		
KW	Zinc-finger.		
SQ	SEQUENCE: 589 AA; 66777 MW; E6812FF3EA34142 CRC64;		
Query Match	6 7%	Score 486; DB 11; Length 589;	
Best Local Similarity	27.8%	Pred. No. 3e-26; 186; Indels 138; Gaps 23;	
Matches	154;	Conservative 75; Mismatches 97	
Qy	41	EEQKERAQKOKGYNQSMQREAKRKTFTVYEPSSWIP--QEMAAAGYFTGKSGIQC	97
Qy	12	KENKE-KMYDFSC-----LYRMSTSAFGRGPVRSIARAGYYTGNDVKC	62
Db	98	FCCSILFSGAGLTRIPIEDIKRFHRDCGGC---LINKDVNIKYDIRVN-----	144
Db	63	FCCGIMLDNNKOGDSPTKEHROFSCSFVOTLSSGGLQSAKNTSPAKSRFAHSPLQ	122
Qy	145	-----LKR-----LRGKMRY-QEEARLASFRNWFYQGISCPVLSEAG	185
Db	123	GGIHSLPSNPLNSRKADEFSLRNPSCSYAMSTEARFLSFSYKWP--LSFLSPRELAKAG	180
Qy	186	FVFKCOPDVFSCGGCAGNWEGDPPWIKHAWPCKEFLASKSSEITQYIOSKG	245
Db	181	FYIITGPDRVACFAGGKLSNWEPPNDPDLPLSERRHHPCHPLFLENTSETORFS-----	232
Qy	246	FVDITGEHFVNSWORELPMASAYCNDSTFAYEELRDSLKDWPRESAVGAALAKAGLF	305
Db	233	-----VSNLSMOT-----HSARMSTFLYWPSSVLVPEOELASAGFY	268
Qy	306	YTGKDIVOCFSCGGCAGNWEGDPPWIKHAWPCKEFLASKSSEITQYIOSKG	245
Db	269	YVDHNDVCFCCDGGLRWEPGDPWIKHAWPCKEFLIRMGQ-EVDEIQARYPHL	327
Qy	365	CELLETTSSNLEDIAVGPPIVEMAQGEHOWEAKNIEOLRAYTASFRHMSLDI	424
Db	328	LEQLISTSDTSEEEN-ADPPVWHGPGE-NW-EDAVMTPTVKA-----	369
Qy	425	SSDLATDHLLGCDSIASHKISKPVQEPLVLPVEFGNLNSVMCV-----EGENG	473
Db	370	----ALD--MGFSRSILVRQIVQVORI--LATGENRTVSDIVSALLNAEDERREKEKERQ	420
Qy	474	SGKTVLKKIAFLWASGCCPPLNRQVFLVYLISSTRPDEGLASICDQOLKEGSYSTEM	533
Db	421	SEET-----ASGDSLIRKNRMALFOQLTCVIP-----ILDLL-BASVLT	461
Qy	534	CMRNITIQLKNOV 546	
Db	462	EEDHDIRQ-KTOI 473	
RESULT	4		
Q9ES9		PRELIMINARY; PRT; 602 AA.	
ID	Q9ES9		
AC	Q9ES9;		
DT	01-MAR-2001 ("TREMBLel. 16, Created)		
DT	01-MAR-2001 ("TREMBLel. 16, last sequence update")		
DE	INHIBITOR OF APOPTOSIS PROTEIN 1.		
OS	Rattus norvegicus (Rat).		
OC	Mammalia; Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Euteleostomi; OX		
NCBL-TAXID=10116;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Holick M., Lefebvre C.A., Hicks K., Korneluk R.G.;		
RT	"Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes."		
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.		
DR	EMBL; AF183430; AAC22970.1; -.		
DR	HSSP; Q13490; 10BH.		
DR	InterPro; IPR001370; BIR.		
DR	InterPro; IPR001315; CARD.		
DR	InterPro; IPR001841; Znf_finger.		
DR	Pfam; PF00653; BIR; 3.		
DR	Pfam; PF00619; CARD; 1.		
DR	Pfam; PF00097; zf-C3HC4; 1.		
DR	SMART; SM00184; CARD; 1.		
DR	SMART; SM00184; RING; 1.		
DR	PROSITE; PS01182; BIR_REPEAT_1; 3.		
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.		
KW	Zinc-finger.		
SQ	SEQUENCE: 602 AA; 67326 MW; CC91385EEA62DE5A CRC64;		





DR	INTERPRO; IPR001841; Znf_ring.
DR	Pfam; PF00653; BIR; 3.
DR	Pfam; PF00097; zf-C3HC4; 1.
DR	SMART; SM00238; BIR; 3.
DR	PROSITE; PS01282; BIR_REPEAT_1; 1.
DR	Zinc-finger; BIR_REPEAT_2; 3.
KW	Zinc-finger.
SQ	SEQUENCE 501 AA; 56578 MW; 4863F69FF2E0C8CD CRC64;
Query Match	5.7%; Score 416.5; DB 11; Length 501; Best Local Similarity 28.3%; Pred. No. 2.2e-21; Matches 119; Conservative 60; Mismatches 162; Indels 79; Gaps 12;
QY	60 EAKRLKTFVTPEPSSWIPOEMAAGFYFVGKSGIOPCCSILIFGAGLRLPIED-- 116
Db	26 EFNRLKTFNPSSPVASASTLARAGFLYGETVQFCFSCH----AADVWQYGSV 80
QY	117 --HKRHPDGGFL----- 196
Db	117 --HKRHPDGGFL----- 196
QY	81 GRHRISPNCRFINGFYFENGATOSTSPGIQNYQKSENCVGNRNRHADREFSHADYL 140
QY	140 IR--VKNLKSRIGGMRYOEEEARLASFRMRPPYVOGICPCVISEAGEFVFTGQDTVO 196
Db	141 LRTQGVVSDTYPNRPAMCSEARKTKEPDWYAH-LSPRELASAGLYTGIDQV 199
QY	197 CFSCGGCLGNWECDDPWKEAHAWPCKEELRSKSSEETIQYIOSYKGFDTGHEFVN 256
Db	200 CFCGGKLKWKWFCDRAWSEHHRHFPNCFFVLRN-----VNYSSEGVS 244
QY	257 SWOERLMASYCNDISFAYEFLRUDSKWPRESAVGVAALAKAGLRTGKDIVCF 316
Db	245 S--DRNPNSTNSPRNPALEYDARIVFTW--LYSNRNEQALARAGFVALGEGDVKCF 300
QY	317 SGCGCLEKWOEGDDPLDHTRCFPNCPTLQNMKSSAEVTPDIOSRGECLELLTSE-- 373
Db	301 HCGGLTDWKPSEDPWEQHAKWVQGCKYLDEKQ--EVINNTHLSIGESVRAEKT 373
QY	317 SGCGCLEKWOEGDDPLDHTRCFPNCPTLQNMKSSAEVTPDIOSRGECLELLTSE-- 373
Db	360 SVTKKIDDTIQFQNPVOEAIRMGFNFKDIIKTTWEEKLQ--TSGS-NYLSLEVLIADVS 415
QY	374 --SNLDSIAVGPVPEMAQEAOWFOEAKNNEOLAAUTSASFRIMSTJDISLAT 430
Db	360 SVTKKIDDTIQFQNPVOEAIRMGFNFKDIIKTTWEEKLQ--TSGS-NYLSLEVLIADVS 415
RESULT	9
Q9ESFO	PRELIMINARY; PRT; 496 AA.
AC	Q9ESFO;
DT	01-MAR-2001 (TREMBUREL, 16, Created)
DT	01-MAR-2001 (TREMBUREL, 16, Last sequence update)
DE	01-DEC-2001 (TREMBUREL, 19, Last annotation update)
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI_TAXID=10116;
RP	SEQUENCE FROM N.A.
RA	Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.; Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes.; Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RT	"The apoptosis inhibitor ch-TAPI is a direct transcriptional target of v-Rel and c-Rel;"
RT	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF311289; AAG42316.1; -.
DR	HSSP; Q13490; 10BH.
DR	IntePro; IPR001370; BIR.
DR	Pfam; PF00653; BIR; 3.
DR	SMART; SM00238; BIR; 3.
DR	PROSITE; PS01282; BIR_REPEAT_1; 1.
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.
QY	60 EAKRLKTFVTPEPSSWIPOEMAAGFYFVGKSGIOPCCSILIFGAGLRLPIEDHRR 119
Query Match	5.3%; Score 386; DB 13; Length 324; Best Local Similarity 28.6%; Pred. No. 1.8e-19; Matches 95; Conservative 41; Mismatches 108; Indels 88; Gaps 7;

Db	30 ELYRMSTFSIIPNVVPSERRLARAGFYYTGQDKVKVFCSCGLVLIDNQPGDNAMEKKHQ	9	Oy	332 LDDHTRCFPNCPELQNMKSAEVTPDLSRGELCELTSESNELESDIAVGP	384
Oy	120 FHPDCGFLIN-----	-----	-----	-----	-----
Db	90 VYPSCSFVQNMLSLNNLGLSTHAFSPPLVASNPSLRSMTLSPSFEQGYFFGSFSSFP	149	Oy	136 -----AKYDTRVKNLRSRGGMRYQEEREARLASFRWMPFYQG1ISPCVLSAGFVF	188
Db	150 QDPVITRAEDL--SHLRSKLHNPSM--SPEEARLTFHAWP--LMFLSTELAKAGLYY	203	Oy	189 TGKQDPTWOCFGGGCLGNWRGGDPWKEHAKWPKCEFLASKSSEETQYIQSYKGFD	248
Db	204 LGTADKVKACFTCGGQLSNWERKDNDAMSEHRHHFPPCPFPVFN-----	-----	Oy	249 ITGEHEVNSWTORELPMASAVCNDSFAYEFLRLSPKDPRESAVGAALAKAGLFYTG	308
Db	245 -----;-----;-----;-----;-----;-----;-----;-----;-----	-----	Oy	309 IKDIYQCFSCGGCLEKWKQEGDDPLDDHTRCFF 340	292
Db	293 RNDVVKFCGCCDGGLRCWESGDDPWEHAKWPF	324	RESULT	11	0960U3
			PRELIMINARY;	PRT;	0960U3
AC	0960U3;				PRELIMINARY;
DT	01-DEC-2001 (T-EMBLrel. 19, Created)				PRT;
DT	01-DEC-2001 (T-EMBLrel. 19, Last sequence update)				498 AA.
DE	LD34777P.				
GN	IAP2.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterigota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydriidae; Drosophilidae; Drosophila;				
OX					
RN	{1}				
RP	SEQUENCE FROM N.A.				
RC	STRATNEY, CN BW SP;				
RC	Stapleton M., Brookstein P., Hong L., Agbayani A., Carlson J.,				
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,				
RA	Nunoo J., Parleb J., Paragas V., Park S., Phouanenavong S., Wan K.,				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL: AK051844; EMBL: AK051844; GenBank: CRC64;				
SQ	SEQUENCE FROM N.A.				
Query Match	4 4%; Score 336; DB 5; Length 498;				
Best Local Similarity	27.8%	Pred. No.	1. 3e-15;		
Matches	98; Conservative	Mismatches	54; Indels	125; Gaps	13;
Oy	57 MRESEARKLKTEVTYEEYSWMPQEMAAGGFTGKRSGIQCCFCSSIL-----FGAGITRL	112	Oy	82 AAAGFYFTGKWSGIQCCFCSSILFGAGLTLRIPIEDHKRFHDPCGFLNNKVGNIAKYDIR	141
Db	6 MELESLATRFGEWLPNAPVSAEIDLWANGFATPAKWLAEBCFHCHVRIDRWYEYGDVA--	63	Db	1 AAAGFYFTGKWSGIQCCFCSSILFGAGLTLRIPIEDHKRFHDPCGFLNNKVGNIAKYDIR	60
Oy	113 PIEDHHRHPPCGFLINKD-VGNIAKYDIRKVKLNSRLRGKMRQEEEA-----	161	Oy	142 VKNLKSRLRGKMRQEEREARLASFRN	168
Db	64 -ERHRSSPICSMYLAPNIGGNP-----RSQSDNEENSWDSPESCCPDILEAN	115	Db	61 VKRPERMLRGKARYHEEARLESFED	87
Oy	162 RIASFRNWPYVQG1SPCVLISEAGEVFTGKODTVOCAFSCGCGLGWNWEGDDPWPKEHAKWF	221	Oy	82 AAAGFYFTGKWSGIQCCFCSSILFGAGLTLRIPIEDHKRFHDPCGFLNNKVGNIAKYDIR	141
Db	116 RLVTFKDWMP--NPNTPOQALAKAGFTYLNRLLDHVCWCVNGVIAKWEKNDAFEHKRF	173	Db	1 AAAGFYFTGKWSGIQCCFCSSILFGAGLTLRIPIEDHKRFHDPCGFLNNKVGNIAKYDIR	60
Oy	222 PKC-----EFILSKKKSEELTOYIOSKGFVDTGSHFWVQRELPMASAY-CN	271	Oy	142 VKNLKSRLRGKMRQEEREARLASFRN	168
Db	174 PQCPRVQMGPLIEFATGKMLE-----LGIOPT-----LPLRPKYACV	212	Db	61 VKRPERMLRGKARYHEEARLESFED	87
Oy	272 DSIFAYEELRSDFKDMPPRESAVGAVALAKAGLFYTGKIDIVOCSCGGCLEKWKQEOGDDP	331	RESULT	13	091A70
Db	213 DA-----RLRFTDWPISNQIOPASALAGAGLYYQKIGDQYRCPHNTGLRSQKEDEP	265	PRELIMINARY;	PRT;	091A70
Oy	SEQUENCE FROM N.A.				

RC	STRAIN-BREED LEIGHORN; TISSUE=SPLEEN;		
RX	MEDLINE=21158006; PubMed=11261557;		
RA	Zhou H.; Liu W.; Lamont S.J.		
RT	"Genetic variation among chicken lines and mammalian species in specific genes";		
RL	specific genes";		
DR	EMBL; AF221082; AF25319.1; -.		
DR	HSSP; 013490; IQBH.		
DR	InterPro; IPR001370; BIR.		
DR	Pfam; PF00653; BIR; 2.		
DR	SMART; SM00238; BIR; 2.		
DR	PROSITE; PS01202; PROSITE; PS50143; BIR_REPEAT_1; 2.		
FT	NON_TER 1 1		
SQ	SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;		
Query Match	Best Local Similarity 4.4%; Score 323.5; DB 13; Length 195; Matches 72; Conservative 29; Mismatches 63; Indels 41; Gaps 7;		
Matches 72; Conservative 29; Mismatches 63; Indels 41; Gaps 7;	Query Match	Best Local Similarity 35.1%; Pred. No. 2.5e-15; Matches 72; Conservative 29; Mismatches 63; Indels 41; Gaps 7;	
QY	46 RAKMQGYNQSMSEAKRKLTKTFVYEPSSWIPQEMAAGFTGTGVSGIQCFCSSLILF 105		
Db	19 RSKL--HNPSMSTEEARLRTFHAW-PLMFLSPTELAKAGLYLGTDKVKACFTC--- 69		
QY	106 GAGITRUPIED----HHRFPDCGFLINK-----DVGNTIAKYDIRVKNLKSRLRGK 153		
Db	70 GGQLSNWPKDNAMSEHRRHPPCFEVNLMRQDOPSFENVSNT----- 112		
QY	154 MRYQEEEARLASFRNNWFYVQGICSPCVLSEAGVFTGKQDFTQCCSGCGCIGGNWEGDDP 213		
Db	113 -MQTHEARKVTFINWPTTRIP-VOPEQLADAGFFYYVGRNDDVKCFCGDLRQWEWGDDP 169		
QY	214 WKEHAKWPKPCFLRSKSSSERTQ 238		
Db	170 WIEHAKWPKPCFLRSKSSSERTQ 194		
RESULT 14	RESULT 15		
Q9IA69	PRELIMINARY; PRT; 197 AA.	Q9IA69	PRELIMINARY; PRT; 87 AA.
ID	Q9IA69	ID	Q9IA69
AC	009119	AC	009119
DT	01-OCT-2000 (TREMBlrel. 15, Created)	DT	01-JUL-1997 (TREMBlrel. 04, Created)
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)	DT	01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE	INHIBITOR OF APOPTOSIS 1 (FRAGMENT).	DE	NEURONAL APOPTOTIC SEQUENCES INHIBITOR PROTEIN RELATED SEQUENCE 1 (FRAGMENT).
OS	Gallus gallus (Chicken).	OS	BIRC1-RSL OR NAIP-RSl.
OC	Archosauria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX	OC	Mus musculus (Mouse); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	[1]	RN	[1]
RP	SEQUENCE FROM N. A.	RP	SEQUENCE FROM N. A.
RC	STRAIN=129/SVJ;	RC	STRAIN=129/SVJ;
RX	MEDLINE=97131520; PubMed=8975718;	RX	MEDLINE=97131520; PubMed=8975718;
RA	Scharff J.M., Demron D., Friseilla A., Bruno S., Beggs A.H., Kunkel L.M., Dietrich W.F.	RA	Scharff J.M., Demron D., Friseilla A., Bruno S., Beggs A.H., Kunkel L.M., Dietrich W.F.
RT	"The mouse region syntentic for human spinal muscular atrophy lies within the Lgnl critical interval and contains multiple copies of Naip exon 5;"	RT	"The mouse region syntentic for human spinal muscular atrophy lies within the Lgnl critical interval and contains multiple copies of Naip exon 5;"
RL	Genomics 38:405-417(1996).	RL	Genomics 38:405-417(1996).
DR	EMBL; U6624; AAC52672.1; -.	DR	EMBL; U6624; AAC52672.1; -.
DR	HSSP; 01490; IQBH.	DR	HSSP; 01490; IQBH.
DR	MGI; MGI.10949; Birc1-rsl.	DR	MGI; MGI.10949; Birc1-rsl.
DR	InterPro; IPR001370; BIR.	DR	InterPro; IPR001370; BIR.
DR	Pfam; PF00653; BIR; 1.	DR	Pfam; PF00653; BIR; 1.
DR	SMART; SM00238; BIR; 1.	DR	SMART; SM00238; BIR; 1.
PROSITE; PS01202; PROSITE; PS50143; BIR_REPEAT_1; 2.	PROSITE; PS01202; PROSITE; PS50143; BIR_REPEAT_1; 2.		
FT	NON_TER 1 1	FT	NON_TER 1 1
SQ	SEQUENCE 87 AA; 9958 MW; E601604230BC1D25 CRC64;	SQ	SEQUENCE 87 AA; 9958 MW; E601604230BC1D25 CRC64;
Query Match	Best Local Similarity 4.4%; Score 320; DB 11; Length 87; Matches 60; Conservative 8; Mismatches 19; Indels 0; Gaps 0;	Query Match	Best Local Similarity 4.4%; Score 320; DB 11; Length 87; Matches 60; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
QY	82 AAAGFYFTQWKGJQFCSSLILFGAGITRPLPEDIKRPHPPDCGFLINKDGNIAKDIR 141	QY	82 AAAGFYFTQWKGJQFCSSLILFGAGITRPLPEDIKRPHPPDCGFLINKDGNIAKDIR 141
Db	1 AAAGFYFTQWKGJQFCSSLILFGAGITRPLPEDIKRPHPPDCGFLINKDGNIAKDIR 60	Db	1 AAAGFYFTQWKGJQFCSSLILFGAGITRPLPEDIKRPHPPDCGFLINKDGNIAKDIR 60
QY	142 VKNLKSLRGLRGKHYQEERLASFRN 168	QY	142 VKNLKSLRGLRGKHYQEERLASFRN 168
Db	61 VKSPEKMLRGKGRAYHEEARLESFED 87	Db	61 VKSPEKMLRGKGRAYHEEARLESFED 87

Query Match 4.4%; Score 323.5; DB 13; Length 197;

Search completed: September 30, 2002, 15:06:30

Job time: 186 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on : September 30, 2002, 14:59:19 ; Search time 41.9 Seconds

(without alignments)  
3719.249 Million cell updates/sec

## Title: US-09-830-338-1

## Perfect score: 7308

Sequence: 1 MATQQKASDERISQFDHNL... SKYLTILQKWILPFSPIQK 1403

## Scoring table: Blosum62

Gapext 10.0 , Gapext 0.5

## Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

## Minimum DB seq length: 0

Maximum DB seq length: 2000000000

## Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

A\_Geneseq\_032802:\*

1: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*

2: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*

3: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*

4: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1983.DAT:\*

5: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1984.DAT:\*

6: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*

7: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1986.DAT:\*

8: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1987.DAT:\*

9: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1988.DAT:\*

10: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*

11: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1991.DAT:\*

12: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1992.DAT:\*

13: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1993.DAT:\*

14: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1994.DAT:\*

15: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1995.DAT:\*

16: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1996.DAT:\*

17: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1997.DAT:\*

18: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1998.DAT:\*

19: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA1999.DAT:\*

20: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*

21: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

22: /\$IDS1/geodata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	7308	100.0	1403	Neuronal apoptosis
2	7308	100.0	1403	Gonadotrophic hormo
3	7308	100.0	1403	Human apoptosis in
4	7308	100.0	1403	Human NAIP protein
5	7284	99.7	1403	Neuronal apoptosis
6	6691	91.6	1295	Gonadotrophic hormo
7	6691	91.6	1295	Human apoptosis in
8	6373.5	87.2	1232	Neuronal apoptosis
9	61204	9.0	22	Human caspase recr
10	654	8.9	1070	Amino acid sequenc
11	653	8.9	22	Human caspase recr

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

## RESULT 1

ID AAW20032 standard; Protein: 1403 AA.

XX AAW20032;

XX DT 06-OCT-1997 (first entry)

DE Neuronal apoptosis inhibitor protein (NAIP),

XX KW Neuronal apoptosis inhibitor protein; NAIP; diagnosis;

KW therapy; cancer; AIDS; amyotrophic lateral sclerosis; spinal muscular atrophy.

OS Homo sapiens.

XX PN WO9726331-A2.

XX PD 24-JUL-1997.

XX PF 17-JAN-1997: 97WO-1B00142.

PR 19-JAN-1996; 96GB-0001108.

PA (UOT-) UNIV OTAWA.

XX PI Korneluk RG, Mackenzie AE, Robertson G, Roy N, Tamai K,

XX DR WPI; 1997-385335/35.

DR N-PSDB; AAT71265.

PT New neuronal inhibitor of apoptosis - useful for diagnosing and treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis

XX

Rank	Score	Match Length	DB ID	Description
12	566	7.7	841	Murine EST encoded
13	545.5	7.5	118	Human colon cancer
14	536.5	7.3	738	Amino acid sequenc
15	462	6.3	618	Human inhibitor of
16	462	6.3	618	Human apoptosis in
17	462	6.3	618	Human C-IAP1. Hom
18	462	6.3	618	Human HAP-2 prote
19	462	6.3	618	Human cellular inh
20	457.5	6.3	612	Murine c-IAP. Mus
21	457.5	6.3	612	Murine HAP-2 prot
22	441.5	6.0	591	Mouse apoptosis in
23	440	6.0	604	Mouse HAP-1 prot
24	437.5	6.0	496	Mouse apoptosis in
25	437.5	6.0	496	Murine XAP prote
26	436.5	6.0	604	Human inhibitor of
27	436.5	6.0	18	Human c-IAP2. Hom
28	436.5	6.0	604	Human cellular inh
29	436.5	6.0	20	Human XAP-1 prote
30	435	6.0	1141	Human XAP-MLR chi
31	431.5	5.9	496	Mouse inhibitor of
32	431.5	5.9	604	Human XAP protein
33	431.5	5.9	19	Human apoptosis in
34	427.5	5.8	602	Human HAP-1 prote
35	407	5.5	497	Mouse apoptosis in
36	403	5.5	497	Human apoptosis in
37	403	5.5	497	Human XAP protein
38	403	5.5	497	Human apoptosis in
39	354	4.8	642	Human protein sequ
40	340.5	4.7	438	Drosophila melano
41	336	4.6	498	Drosophila inhibit
42	335	4.6	498	Human secreted pro
43	320	4.4	60	Angiotensin conver
44	318.5	4.4	306	Drosophila mutant
45	304.5	4.2	438	



DR N-PSDB; AAX58000.

XX An excessive ovulation animal - useful for improving the  
 PT productivity of animals  
 PT XX  
 PS Claim 3, Page 11-14; 18pp; Japanese.

XX This sequence represents a gonadotropic hormone.  
 CC The invention relates to an excessive ovulation animal, which is a transgenic animal with a totipotent cell containing a DNA fragment containing a promoter sequence and a gonadotropic hormone coding sequence. The DNA fragment is in the somatic cell chromosome. The CC animal is useful for improving the productivity of excessive ovulation animals. The method can improve the productivity of CC animals. The method can improve the productivity of a useful animal.

SQ Sequence 1403 AA;

Query Match	100 %; Score 7308; DB 20; Length 1403;
Best Local Similarity	100 %; Pred. No. 0;
Matches	1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MATQQKASDERISQDHDNLALPESLALLGIDAVQLAKELERBEEQERAKMOKGYNQMRSE 60
Db	1 matqqkhasderisqdfhnlpelssaligldavqlakelereeketakungkgynsqmre 60
QY	61 AKRLKFVTVTEPYSSWIPQEMAAGFYFTGCKSGTQCFCSSLILFGAGLTRLIEDHKRF 120
Db	61 akrktftvtyepysswipqemaagfyftgcksgtqcfcsslifgaglrlpledhkrf 120
QY	121 HPGCGELFLINKDVGNIKAYDIRKVNKLRSRLRGCKMRYQEEARLASFRNWPFPYQGJSPCV 180
Db	121 hpgcgtflinkdvgntakydirknksrltggnkmyrqeeearlastfrnwfpfyqgjspcv 180
QY	181 LSEAGTVFTGKQDTWOCFSGGGCLGSNWEEGDDPWHEAKWPKCERPLRSKKSSEETQYI 240
Db	181 lseagfvftgkqdtqfcggcgclgnweegddpwkehaktfpkceflrskksseitqy 240
QY	241 QSYKGVFDITGEHVFNSWORELPMASAYENDSTIAVEELRUDSTKDWPRESAVVAALA 300
Db	241 qsykgvfditgehvfnswqplmasayendstiaveyeirlsdikdwpsavvaala 300
QY	301 KAGLFVFTGKNDWQFSCGCLEKKMEOGDPDIDTRCFNCPELQNMKSAEVPDQS 360
Db	301 kaglyftgkdnwqfscgcgclekwgddpldhtrcfpncplqnmksaaevpdqs 360
QY	361 RGECELLETTSESNEIDSLAVGPVPEMAQGAQMPEAKNLNEQDRAATTSASFRHMS 420
Db	361 rgecellettsesnledslavgpvpemaqgaqwfqeknlnqraaytsasfrms 420
QY	421 LLDISSDLATDHLCDCDLSTASKHISKPVQBLPLPEVFGNLNSYMCVEAGSKTVLL 480
Db	421 ldissdlatdhlcgdcslaskhiskpvqepivipevgfnlnsynvegeagsktvll 480
QY	481 KKIAFLWASSCCPILNRFOLVYLSUSTRPDEGLASITCDOLLKEGSTEMCARNIQ 540
Db	481 kkiaflwasccpilnrfqvfyislsstrpdeglaicdqlekegsystemcnriq 540
QY	541 OLKNQVLFLDDYKEICCSIPOVIGKLIQKHNHSRFLCLIAVRNARDIRYLETILEK 600
Db	541 qkngyfliddykeicsipqvgikiqkohsrclliaavrtnardiryleik 600
QY	601 AFPFVNWVCLRKLFSHNMTRLKEMVYFGKNOHQRIKQMPFLVAAICAHWFQYPFDPS 660
Db	601 afpfvnytcirklfshnmtrlkfmvfgknqsiqkqtpfvaicahwfqypfdps 660
QY	661 FDDVAVFKSNERLRSRNKAETIKATVSCGEALKGPFSCCEFNDDLAEGVD 720
Db	661 fddvavfkstmrslrsrnkaetikatvscgealkgfscctefnddlaegvd 720
QY	721 EDDTMCLMSKETAQRURPFRFLSPAOEFLAMRIELJDSDROPHDGLYHLKQINS 780
Db	721 eddtmclmsktaqrurpfrflspafqeflagmrieliidsdqehdqldgylhylkqins 780

RESULT	3
ID	AY09539
AA	AY09539 standard; Protein: 1403 AA.
AC	AY09539;
XX	
DT	20-JUL-1999 (first entry)
XX	
DE	Human apoptosis inhibiting protein #1.
XX	
KW	Human; apoptosis inhibitory protein; apoptotic disease; diagnosis; spinal muscular atrophy.
XX	
OS	Homo sapiens.
XX	
PN	JP1116599-A.
XX	
PD	27-APR-1999.
XX	
PF	14-OCT-1997; 97JP-0280831.
XX	
PR	14-OCT-1997; 97JP-0280831.
XX	
PA	(KAGA-) KAGAKU GIJUTSU SHINKO JIGODAN.
XX	
DR	WPI; 1999-323531/27.
N-PSDB;	AAX56272.

XX  
PT New apoptosis inhibitory protein - useful for determining mechanism  
PT of various apoptotic diseases e.g. human spinal muscular atrophy  
XX  
PS claim 1; Page 4-8; 16pp; Japanese.  
CC The present sequence represents a human apoptosis inhibitory protein.  
CC the mechanism of various apoptosis diseases such as human spinal  
CC muscular atrophy and the diagnosis, the prevention and the treatment  
XX of such diseases.  
SQ sequence 1403 AA:

Query Match

Best Local Similarity

Matches

1403;

Conservative

0;

Misnatches

0;

Indels

0;

Gaps

0;

OY

1

MAYQQKASDERISQDFNHNLBPELSALIGLDPAAVQLAKELREEDERAKMQGINSQRSE

Db

1

matcqqkaderisqdfnhnlpeisaliglida

OY

61

AERLKKEFVTPYPRSSYPOEMAAAGFYFTGVKSIQOCRCSLILFGGLTRPIEDHKF

120

61

akrikktvtpyprssyppqggmaaqgfyfgkvkgqiqccsllfagiltrpiedhkf

QY

121

HPDCGGFLNLNDGNGNAYDIRVKNUKSRLURGRMRYRREEALASFRNWPYVOGSTPCV

Db

121

hpdcgflnlndgngnaydirvknuksrlurgrmryreelaskrnlksrlrgkmryqeeearlastrnwnpvqgqpcv

QY

181

LSEAFVFVKGQDPMQSCGGCNGNBERGDDPKELAKWPFCKEELRSKKSERIOTY

Db

181

lseagfvftgkqdtvgqfcsgcglgnweegddpkewhakwipkeflrskseitpy

QY

241

OSYKFVDITGEIRVNSWVQRLPMSACYNSIFAYEEURLSKDWPRESAVGVALA

Db

241

qsyqfvdtqfetgvfnvwqrpelmasaychositayeeirlstfkdwpresvvaia

QY

301

KAGLYFTGKDQVCFSGGCELEKKGEGDOPDLDTTRCPNCPPQLQNMKSSAVENTPQ

Db

301

kaglyftgkdqvlqcfcsgcglekwegdaplhdtrcfpnclfqnkkssavtptqls

QY

361

RSLCILETTESESNFEDSTAVGPVPEMAQEAMQGEAQWPAKNAINEQURAYASERHMS

Db

361

rqelcelletsesnfedstavgpvpeaqwpeakeknegiraytsasrhms

QY

421

LUDISSDLATDHLUCGDLSTASKRISKPVQEPYLPEVGLNSVMCGVEGAGSGTVL

Db

421

ludissdlatdhlucgdlstaskriskpvqepylpevgl

OY

481

KKARLWASGCCPLUNROLVEFLSLSSTRPDEGLASICQOLLEREGSYTEMNRNITO

Db

481

kkafiwsgccplunrqivlylsistrpdeglasicqol

QY

541

QKKNVLFULLDDKEICSIPOVIGKLIOKHNLSRICLLIAVRTNARDIRRUYLTILEK

Db

541

qkhnqvlflldkelsipsqvgiklqhnhsrlcellavrtrardiryleik

QY

601

AEPFYNTVCILRFLFNSINTRKRFMVFGKNSIQKLOKTPUVAATCAHWYOPPDPS

Db

601

affytntvcilrkfshnmtrkrkvfkgknqslqktpjfvaaicahwqrp

QY

661

FQDVAVKSYMERLSLRNKATAELKATVSSCGELAKGFFSCCFEFNDDLAEGYDED

Db

661

fdvvavkfsymarlslrnkataelkatscgalakgffscfcferndddlaegyded

QY

721

EDLTMCMLMSIFTAQRLRPRYRFLSPAFOEFLAGMRLIELLDSDRQEIQDGLYHJKQINS

Db

721

editinglmksitagrqlrpfrfispaefafcgmlmellusdrqhqdlyhjkqins

QY

781

PMMTYSAYNNFLNVSSLPSTKAGPKTVSHLHLVDKESLENISUNDYILKHOEISIQ

840

XX

Db 781 pmmtvsaynnflnysslpstkagpkivshlhlyankeslenisenddylkhpelslq 840  
QY 841 MQLRGLNOICPOAYFSVNSELIVALKTYQSVTVAACSPFVLFQFLGRTTTLGAINL 900  
Db 841 mqllrgiqwicpqaysfmvsehnlvialktaygntvacspfqlfqrtitgalm 900  
QY 901 QFFDHPESSLSLRSHFPTRGKTSPRAHFSVLETCFDKSOVPTDODYASAFEPINEW 950  
Db 901 qyffdhpesilsrlsifprlnqtsprahfsvletcfokscqytdqdyasafepinew 950  
QY 961 ERNLAKEDBNKSYMDMORASPDISTCWKWLSPKQYKIPCLFVDVNDIDVQDMLEI 1020  
Db 961 ernlaekedvksydmqraspistgywklspqkicpiclevdvndvqgqamleil 1020  
QY 1021 MTVFSASQTELHJNHSRFRFIESIRPALELSKASVTKCISLLESAEBLLLPSIE 1080  
Db 1021 mtvfeasqsrqsfqslhnsqfriesirpaleskavsktsklesaaedellitlpsie 1080  
QY 1081 SLEVSQTGOSDOPPNIDKFLKERSDLEGNNINVFSVPEEPFNFMHEKLIOTSA 1140  
Db 1081 slevsgtqsdqsfidpnlakfickelsvdsdlegninvfasripeepnfhmekliotisa 1140  
QY 1141 EYDSKLVRILLIONSPNHPFHCKCNFSDCSLMMVLVSKKLBKIKSDSEFOAVPVA 1200  
Db 1141 eyopskivklqkqspnphlkhkntfsdgsimtlvskkiteiksdfrqavpva 1200  
QY 1201 SLDNFISIKLUMLEGOPPDETERSEFAVYLGSUSLNELELILPQPGDGYRVALQKTOCO 1260  
Db 1201 sfpnfisklinleqgpfetecktskfaxylslnleelilpdydlyrvalkiqcc 1260  
QY 1261 OHCRLVLSFKTLNDSVWEIAKVAISGPKOLENLKSNIKRTEGYNFEQALDM 1320  
Db 1261 qhclvrlsftklnodsvveiakvaissqgfqklenklsinhkiteegyrnfqaldm 1320  
QY 1321 PNQLEIDISHHFTECIKADTTWLSOCVRLPRLIRLMULSWLADDALLNWKER 1380  
Db 1321 pnlgeldishrteckqattvkslsqcvrlprirlnmlswladdallnwkern 1380  
QY 1381 HPOSKYLTQOKWLPSPIQK 1403  
Db 1381 hpsqskyltilqkwlpfspiqk 1403

RESULT

4

AYY8053

ID AYY8053

standard:

Protein:

1403 AA.

XX

AC AYY8053;

XX

DT 22-SEP-2000 (first entry)

DE Human NAIP protein.

XX

NAIP:

apoptosis inhibiting protein; monoclonal antibody; diagnosis;

treatment; human.

KW

apoptosis disease onset mechanism; drugs development; prevention;

XX

OS Homo sapiens.

XX

Key

Region

Location/Qualifiers

226..586

/note= "Immunogenic region, specifically described

in Claim 1"

Region

841..1052

/note= "Immunogenic region, specifically described

in Claim 1"

PH

W020024889-A1.

XX

04-MAY-2000.

XX

22-OCT-1999.

99WO-JP05841.

XX

PR 26-OCT-1998; 98JP-0304550.  
XX  
PA (NISCA-) JAPAN SCI & TECHNOLOGY CORP.  
PA (SAKAI/) SAKAI H.  
XX  
PI Sakai H., Ikeda J.;  
XX DR WPT; 2000-350731/30.  
XX N-PSSDB; AAA358808.  
XX  
PT simple and accurate quantitation of human apoptosis inhibitory protein  
PT (NAIP) with monoclonal antibodies, for disease diagnosis and  
development of drugs to prevent and treat apoptosis-related diseases -  
XX  
PS claim 1; Page 24-30; 36pp; Japanese.  
XX  
CC This invention describes novel anti-NAIP monoclonal antibodies, produced  
CC by hybridomas, prepared by fusing antibody-producing cells of mammals  
immunized with an immunogen containing residues 256-586 or 841-1052 of a  
CC 1403 residue amino acid sequence, fully defined in the specification, or  
CC their partial sequence, with a myeloma cell line. The monoclonal  
CC antibodies are for the study of apoptosis disease onset mechanism,  
disease diagnosis and development of drugs to prevent and treat  
CC apoptosis-related diseases. The quantitation method with the monoclonal  
CC antibodies is simple and accurate by using a biological specimen. This  
CC sequence represents the human apoptosis inhibitory protein NAIP which is  
described in the method of the invention.  
SQ Sequence 1403 AA:  
XX

Db 541 qlnqyvfliddyekeicsipqvigkliqkhnsrtcellavtnrardirylelik 600  
 Qy 601 AFPFYNTVCLRKLSHNMTRKEMYFCKKNQSOKIOTPEVAACAHWQYFEDS 660  
 Db 601 ||||||| afpfyntvcirkfshomtrlkfmwfgknqsokiqgtpivaaicahwqyfcdps 660  
 Qy 661 FDDAVFKYSWERLSRNKATAELIKATUSSCGELALKGFFSCCFEFNDLDAEGYDDE 720  
 Db 661 ||||||| fddavfkysmerlsrnkataelikatvsscgelalgkgffsccefndldiaeagded 720  
 Qy 721 EDLTMCUMSKTQAQRPRFRFLSAFOERLAGHLIELDSQDQEHDGLYHLQINS 780  
 Db 721 ||||||| editmcumskitaqtqrprfrflsafoerlaghlieleldsrdqehdgllyhlkins 780  
 Qy 781 PAMTVASYNPLNYSSLPSKTAGPKIVSHLHVLDNKFESLENSENDYLYKOPETSLQ 840  
 Db 781 ||||||| pmutvaysnplnysslpsktakgpkivshlhlvdnkfeslenendylykopeisq 840  
 Qy 841 MOLLRGWOCQPAQYFSMVEZBLLYLAIKAYQNSNTVAACASPFVLFQLOGRTLTGALNL 900  
 Db 841 ||||||| mqllrglwqcpqayfsmvsehlvlalktayqntvaacspfvlfqlogrtitgalm 900  
 Qy 901 QVFDFHPESSILRSRTHPFLRGKNTSPRAHSVLETCFDKSQVPTIDQDYASAFPMNEW 960  
 Db 901 ||||||| qvfdhpesilrsrhfpigrnksprahfsveitcfdksqptidqdyasafpmnew 960  
 Qy 961 ERNLAKREDVYKSYMDMORASPDUSTGKWLSPKQYKPCLEYDWDNPDTWQGDMLEIT 1020  
 Db 961 ||||||| enlaekdnvksymdqraspdustgwkspkqykcpcleydvdndvvgdmleit 1020

OS	Homo sapiens.
XX	
FH	
KEY	Location/Qualifiers
Misc-difference	600
FT	/note= "encoded by AAA"
Misc-difference	919
FT	/note= "encoded by CCA"
XX	W09726331-A2.
PD	24-JUL-1997.
XX	
PP	17-JAN-1997; 97WO-IB00142.
XX	19-JAN-1996; 96GB-000110B.
XX	(UYO-) UNIV OTTAWA.
PA	
XX	
PI	Korneluk RG, Mackenzie AE, Robertson G, Roy N, Tamai K;
XX	WPI: 1997-385335/35.
DR	WPI: AAT71266.
XX	
PT	New neuronal inhibitor of apoptosis - useful for diagnosing and treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis
XX	Claim 41; FIG 7A-L; 102pp; English.
CC	Novel human neuronal apoptosis inhibitor protein (AAW20033), or NAIP, is a negative regulator of apoptosis, partic. neuronal apoptosis and, when deficient or absent, contributes to neurodegenerative phenotypes such as spinal muscular atrophy (SMA) and amyotrophic lateral sclerosis. Its amino acid sequence was deduced from a cDNA clone (AA71266) obid. From a human foetal spinal cord cDNA library. NAIP polypeptides, esp. those containing at least two CCR (baculovirus IAP repeat) domains, can be expressed in host-vector systems and used to increase or induce apoptosis for the treatment of AIDS, neurodegenerative disease, myelodysplastic syndromes or ischaemic injury, to screen for (ant)agonists, or to produce antibodies useful for inhibiting apoptosis.
CC	syndromes or ischaemic injury, to screen for (ant)agonists, or to produce antibodies useful for inhibiting apoptosis.
CC	sequence 1403 AA;
SQ	
Query Match	99.7%; Score 7284; DB 18; Length 1403;
Best Local Similarity	99.7%; Pred No 0;
Matches	1399; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Oy	1 MATOOAKASDERIQDFHNLPELPSALGLDAVOLAKLEEESEQKERAQMKQGYNQNSMRSE 60
Db	1 matcqkaderisqdfnlpepsalglidaqvlaekleeeeqkerakngkgynsqmse 60
Oy	61 AKRURKTFVYEPSSWIFQEMAAAGEYFTCVKSGIQCFCSSLICAGLRLTRLPEDHKRF 120
Db	61 akriktfvtyepsswipqemaagftgvgksqiqfcfcslilqtagitrglkrf 120
Oy	121 HPGCGFLINKDVGNIAYKDIWVKNLRSRGKMRQEABLASFRNRPFYQGISRCV 180
Db	121 hpdcgflinkdvgnlaikydrvknsrsrqgkmyqeeearlafsnspfyqgicpv 180
Oy	181 USPAGFVFTGKOPDTCFCGGCLGNWEEGDPKNEHAKWPKPKEFLRSKSBEBTOYI 240
Db	181 lseagfvrtgkqdtvcfcsgcgclgnweeddpwkeahwfkpcqefisksksseeltcyi 240
Oy	241 OSYKGFDVDTGEHFWNSWVORBLPMASAVCNDSTFAAYERBLRUDSPKDMFRESAWGVALA 300
Db	241 qsykgfdvdtgehfvnswwqrelomasayendsfayeerlidsfkowpresavgala 300
Oy	301 KAGLRTGIDIVOFSCCGCQLEKMQEGDPLDDHTPNCFLPQNMSSAEVTPLQS 360
Db	301 kaglytgikdivofscggclekwqegddpldhtcfnpcflqnmksaaevtpdls 360
Oy	361 RGECELLETTSESNLEDSTIAVGPIVPEMAQGEAQWFOEAKNNEQQLRAATSAFSFRHMS 420
DB	361 rgecellettsesnledstavgpilpemaaqgeawqfqgeaknlnqeqrlayrasfrhms 420
Oy	421 LLDISDLATHLGCDLSTASKHISKPQEPULPEFGNLUSVMCEAGEAGSKVLL 480
Db	421 lidisdlathlgcdlasiaskhiskpqpqevlpvevgninsmvgeageasgkvl 480
Oy	481 KKIAFIWASGCCPLNREFOLVFYLSLSRDPGGLASTICDQOLEKEGSVTCMNRNIIQ 540
Db	481 kkiafiwagccplnrfqldvlysisattpagiasinidqleregsvtcmnrniiq 540
Oy	541 OLKNQYLFLLDYKEICSPQVIGKLQKHNLSRTCLIAVRTRNARDIRYLETILEK 600
Db	541 qiknqvlifddykaicsipqvlqklqkhisrtclilavtnrardiryletiled 600
Oy	601 AFPYNTYVCLRLKFHNTTRKFMVFGKNSLOKIQKPLFVAICAHWFQPFDS 660
Db	601 afpnyntvcilrkfshomtrirkfmvfyfgknqslqkqkplfvaicahwfqpfds 660
Oy	661 FDDAVAFVSYMERLSRNKATEILKATVSSGELALKGFSCCDEFNDDELAENGVD 720
Db	661 fddavavfsymerslrnkataeilkatvatvssgelalkgfrsccliefdddeagvd 720
Oy	721 EDTCMCJMSKFAQRUPLPYRLSPAFQEFAGMRTEFLDSRQEHQDGLYHLQINS 780
Db	721 editmcjmskfaqrupryrlspafqefagmrtefldsrqehqdglyhlqins 780
Oy	781 PMTVSYANNFLNYVSSLPSRSTKAGRIVSILHVNKESENSENDYLUKQPELSLQ 840
Db	781 pmtvasyannflnyvsslspsrskagrivsilkvhilhvankeilen sendylikhgpeisq 840
Oy	841 MOLLRGJWQICPQAYSMVSWEHLVLAALKAYOSVTAACSPFVLQFLOGRTLTGALN 900
Db	841 mqllrglwqicpqaysmvswehllvialktayqntvacsfpvlfqflqrttgln 900
Oy	901 QYFFDHPESISLRLRIHPRGRNKTSRPHSFVSLCTEDKSOVTLQDMAFEPANEW 960
Db	901 qyffhpesislrlsinfslrgntsprahsfvslctcfokskqyptqdysafepnew 960
Oy	961 ERNLAKEDKVSKNDMORRASPOLSTGCKWKLSPKQK1PCLEVDVNDIDVGQDMLEL 1020
Db	961 ernlakedkvskndmorraspolstgckwklspkqk1pclevdvndidvgqdmlel 1020
Oy	1021 MTVSASORIELHLHNSRGFIESIRPAELLSKAVTKCSISLELSAEOQMLLTPSL 1080
Db	1021 mtvisasqrlelhnhsgfiesirpalelkasvtscklesaegelltlips 1080
Oy	1081 SLEYSGTOSQDQIFPNLKDFLKLKEUSVDELEGINTVFSVPEEFFNFHNEKLQISA 1140
Db	1081 slevtsgtqsgdqifpnldkfickelsvdleginvfscippefpnfhmekllqisa 1140
Oy	1141 EYPSKLUKLIONSPNUHVFIKCNFSDFESLMTLVSKRLTERKESPSFFOVPEA 1200
Db	1141 eypskluklionspnahfhikcnfesdfslmlvskchlkfadsfcavpfa 1200
Oy	1201 SLPNFSIKLUNLEGQFPDSETSEKFAYTIGLSNLLEELPTGDTIVRAKLIQOCQ 1260
Db	1201 slpnfisklunlegqqfdetsekfaylgslnleelptgdgylrvakiliqcq 1260
Oy	1261 QHCLRLVSFRKTLANDSVWIAKAYAISGCFOKLENKLISNHNITECGRNFQALDN 1320
Db	1261 qhclrlvsfrktlandsvwiaqayaisgcfoeklenklisnhnitechgrnfqaldm 1320
Oy	1321 PNLQELDISRHFTECTKAOTVLSQYLRURIRLNUMLSLDDAIILNVKMR 1380
Db	1321 pnqeldisrhftecikaatttvksisqgvrlipriirlnmwslladdalnvkmer 1380
Oy	1381 HPSKYLTIQKWLIPFSPIQ 1403
Db	1381 hpskyltiqkwlpfsplq 1403

AYA14080		Db	rgelcellettseasnledslavgvipemaaqeadqvfpeaknlneqlraaytsasfrhms
ID AAY14080 standard; Protein; 1295 AA.		QY	421 LUDISSDATDHLGLGCDLSTASKHLSKPPVDEPLVPEVGFLNNSMVCVEGEAGSGKTULL 480
XX		Db	421 lldisdatdhlglgdslaskhskpvapvlperfglnsmcvgeagegsvtkvll 480
AC AAY14080;		DE	Gonadotropic hormone protein sequence.
XX		DE	Gonadotropic hormone; excessive ovulation animal; transgenic animal;
KW totipotent cell; somatic cell chromosome.		DT	20-JUL-1999 (first entry)
XX		XX	Homo sapiens.
OS Homo sapiens.		XX	JP11113444-A.
PN XX		XX	27-APR-1999.
PD XX		PF 14-OCT-1997;	97JP-0280830.
XX		PR 14-OCT-1997;	97JP-0280830.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.		XX	(KAGA-) SAKAI H.
PA (SAKA-) N-PSDB; AAX58001.		XX	WPI; 1999-320709/27.
PS DR		XX	N-PSDB; AAX58001.
PT An excessive ovulation animal - useful for improving the productivity of animals		XX	Claim 3; Page 14-18; 18PP; Japanese.
XX		CC	This sequence represents a gonadotropic hormone.
CC The invention relates to an excessive ovulation animal, which is a transgenic animal with a totipotent cell containing a DNA fragment containing a promoter sequence and a gonadotropic hormone coding sequence. The DNA fragment is in the somatic cell chromosome. The excessive ovulation animal is useful for improving the productivity of animals. The method can improve the productivity of a useful animal.		CC	containing a promoter sequence and a gonadotropic hormone coding sequence. The DNA fragment is in the somatic cell chromosome. The excessive ovulation animal is useful for improving the productivity of a useful animal.
XX		SQ sequence 1295 AA;	
Query Match 91.6%; Score 6691; DB 20; Length 1295; Best Local Similarity 99.8%; Pred. No: 0; Mismatches 1282; Conservative 2; Indels 0; Gaps 0;		QY 481 KRIAFELWASGCCPLURFOLVFSLSSTRDEGLASICIDOLLKREGSYTEMCHRNTI 540	Db 481 qkknqyklldykeicsipqvgiklikohnslrcellavtrnrdiryleilek 600
QY 1 MATQOKASDESISQFDHNLPELESLAIGLORWQAKELEREEQKERAQMKGYNSOMRE 60		Db 481 kkfiafwsgccplnrqlyfylsistrpbdegiaslidiqlekegsystemcmnliq 540	OY 541 QLKNOVLFELDYKECSIROVIGKLIQKHLSCCLLAVTRNARDIRYLEILEK 600
Db 1 matqokasdesisqfdhnlpelelsaligldavqlakeleeeqkerakmgkynsqmre 60		Db 601 AFPYNYWCILRKLFHNMRKLFVAVICAHWFQPFDS 660	Db 601 afpyntcyirklfhnmtlkfnvfyngsqikqklightplfralaichwfqpfds 660
QY 61 AKRLKFVTFTEPYSSIPQEMAAGFYFTGKKGTOCFCSSLILFGAGLTRLPIDHKRF 120		Db 661 FDDAVAFKSYMLRSRNKATAEILKATVSSGELALKGFSSCCBFNDDLAEAGVDED 720	Db 661 fdovavfkysmerlsrnkataelikatvsscgelaikgfscfcfeendlaeegvd 720
Db 61 akrkfvtfeyppswipqemaagfyftgksglqfcslilgagltripidhkrf 120		QY 721 PMTIVSANNLNTVYSSLPSKAGRIVSHULHLVNEKSENLENTSENDVLYKHQBISLQ 840	QY 721 EDLTMCMSKTAQRLRPFYFLSPFQEFLAGMLIELLSDRGEHQDIGHYHQS 780
QY 121 HDPGCGELLNKDVGNIAKYDIRVKNLMSRLRGKMRQEEEARLASTRNWPFYVOGSPCV 180		Db 721 editmcimskitaqrirpfyrtspfqtqeflagmlielldsdrgehdqihqkqins 780	Db 721 pmmtvaygnfnuyssplskagptkvshilhvdnskenisenddykhpeis1q 840
Db 121 hpdccflinkdvgnakydirkvnksrlkrqkygeearlasrnwpfyqgqspcv 180		QY 841 MQLRGWQICPQAYSMSVBLLVIAKTAQSONTVACASPFWIQFLQGRTLTGALN 900	QY 841 mqlrlgwqicpqayfsmvsehlivalktaqyntsntvacaspfvqflqqrttigaln 900
QY 181 LSEAGKVFTGSKDQTVQCFSCGGCLNWEEDDPWKHAKUPPKCBLRSKSEETQYI 240		Db 901 QYFFDHPESLSLRSHTFPINGNKTSPPRAHSVYLETCFDKSOSVTPIDQDASAERPMEN 960	Db 901 qyffdhpesslsrshtfpirkntsprahsksvletcfdksqvptldqyasafpmew 960
Db 181 lsagkvftgskdqvfcscggclnweeddpwkhaekwkpckfirsksseetqy 240		QY 961 ERNLAKEDKYMKSMMORRASPLUSTGYNLUSPKYKPCOLEVYNDIYVGQMLEIL 1020	QY 961 ernlaakedkymksymqrrasplustgywlspkypkpclevedndidvqgqmlieil 1020
QY 181 lsagkvftgskdqvfcscggclnweeddpwkhaekwkpckfirsksseetqy 240		Db 961 ernlaakedkymksymqrrasplustgywlspkypkpclevedndidvqgqmlieil 1020	Db 961 ernlaakedkymksymqrrasplustgywlspkypkpclevedndidvqgqmlieil 1020
Db 181 lsagkvftgskdqvfcscggclnweeddpwkhaekwkpckfirsksseetqy 240		QY 1021 MTFVSASQRIEHLHNSRGFTESIRPALLESKLSRAEOPBLTPLE 1080	QY 1021 MTFVSASQRIEHLHNSRGFTESIRPALLESKLSRAEOPBLTPLE 1080
Db 181 lsagkvftgskdqvfcscggclnweeddpwkhaekwkpckfirsksseetqy 240		Db 1021 mtvfsasqrlelhnsrgfesirpallesklsraeopbltple 1080	Db 1021 mtvfsasqrlelhnsrgfesirpallesklsraeopbltple 1080
QY 1081 SLEVSTQIISODQDIFPNLKDPLCKLSVLDLEGININVSPVPEEFNFHNEKLQIQA 1140		QY 1081 SLEVSTQIISODQDIFPNLKDPLCKLSVLDLEGININVSPVPEEFNFHNEKLQIQA 1140	QY 1081 slevstqiqsqqifphdickelksvdieglninvspvpeefpnfhmekiliqisa 1140
Db 1081 slevstqiqsqqifphdickelksvdieglninvspvpeefpnfhmekiliqisa 1140		QY 1141 EVDPSKVLKLLONSPNPHFLKCNFSDGSLMTLUSCILKTERKFSSFFQAVPVA 1200	QY 1141 EVDPSKVLKLLONSPNPHFLKCNFSDGSLMTLUSCILKTERKFSSFFQAVPVA 1200
QY 1141 eydpskvlkilqsnplhifvflknctfsdfslmlmtvskkitekfksasifqavpva 1200		Db 1141 eydpskvlkilqsnplhifvflknctfsdfslmlmtvskkitekfksasifqavpva 1200	Db 1141 eydpskvlkilqsnplhifvflknctfsdfslmlmtvskkitekfksasifqavpva 1200
Db 1260 1260 1260 1260		QY 1201 SUPNETSLKILNLEGQOPDEETSEKPAVILGSLSNEELILPTGDIYRVALIQQ 1260	QY 1201 SUPNETSLKILNLEGQOPDEETSEKPAVILGSLSNEELILPTGDIYRVALIQQ 1260
Db 1260 1260 1260 1260		Db 1201 slpnfslskinlegqfpdeetselfayylqslsleelliptgdqiyrvakliiqcq 1260	Db 1201 slpnfslskinlegqfpdeetselfayylqslsleelliptgdqiyrvakliiqcq 1260
QY 1260 1260 1260 1260		QY 1261 QHCLRVLSFFMTLNDSSVETAKV 1285	QY 1261 QHCLRVLSFFMTLNDSSVETAKV 1285
Db 1261 qhclrvlsffktlndssvveigel 1285		Db 1261 qhclrvlsffktlndssvveigel 1285	Db 1261 qhclrvlsffktlndssvveigel 1285
RESULT 7			
Db AAY09340			
XX AAY09540 standard; Protein; 1295 AA.			
AC AAY09540;			
XX 20-JUL-1999 (first entry)			
DE Human apoptosis inhibiting protein #2.			
OY 361 RQELCELLETTSESNLLEDSTAVGPITVPEMAQGEAQWQEQAEQNLEOLRAAVTASFRHMS 420			

XX  
 KW Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;  
 XX spinal muscular atrophy.  
 OS Homo sapiens.  
 XX  
 PN JP1116599-A.  
 XX  
 PD 27-APR-1999.  
 XX  
 PR 14-OCT-1997; 97JP-0280831.  
 XX  
 PR 14-OCT-1997; 97JP-0280831.  
 XX  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGODAN.  
 XX  
 WPI; 1999-323531/27.  
 DR N-PSDB; AAX5273.  
 XX  
 PT New apoptosis inhibitory protein - useful for determining mechanism  
 PT of various apoptotic diseases e.g. human spinal muscular atrophy  
 XX  
 PS Claim 1; Page 8-11; 16pp; Japanese.  
 XX  
 CC The present sequence represents a human apoptosis inhibitory protein.  
 CC The mechanism of various apoptosis diseases such as human spinal  
 CC muscular atrophy and the diagnosis, the prevention and the treatment  
 CC of such diseases.  
 SO Sequence 1295 AA;

Query Match 91.6%; Score 6691; DB 20; Length 1295;  
 Best Local Similarity 99.8%; Pred. No: 0;  
 Matches 1282; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MATQQKASDERISQFHNLIPESLPLGIDAVOLAKEEEEDKERAKMKGINSQRE 60  
 DB 1 matqqkasperisqfhnlipeslplgida...lakel...kerakmkginsqre 60  
 OY 61 AKRLKTFVTEPYSSWIPOBMAAAAGFYFYGKVKQIOPCCSLLFGAGLTRPIEDHKR 120  
 DB 61 akrlktfvt...epyswipobmaaaagfyfygkv...q...piedhk... 120  
 OY 121 HDPCGFLINKDVGNATAKDIRVNKLSPRLGERMKYOEERLA...RASRNWEPYVOGTSPCV 180  
 DB 121 hdp...cgflinkdvgnata...r...asrnwe...yvogtspcv 180  
 OY 181 LSEAGFVFPTGKQDNCQCSGCCLGNNREGDOPWKEHAKMPKCELSKKSSETOY 240  
 DB 181 lseagf...ptgkqdncqcs...lgnnregdopwkehakmpkce... 240  
 OY 241 QSKGFVDTGEHFVNNSWQILPMASACNDISFAVEELRUDSKDWRESAVGAALA 300  
 DB 241 qskgf...vdtgehfvnns...wqilpmasacndisfa... 300  
 OY 301 KAGLFYFGIKDIWOCFSCGGCLEKMQEGDPLDPIDTRCPNCPLQLNMKSAETPDIQS 360  
 DB 301 kaglfyfgikdiwocfscggc...lekmqegdpldpidtrcpn... 360  
 OY 361 RQELCCELETTSESNILEDSTAVGPIVPEMAQGEAQWFOBAKNINNEQOLIAAVVSASFRHMS 420  
 DB 361 rqelcce...ttse...ledstavgpi...pe...aqwfo... 420  
 DE Neuronal apoptosis inhibiting protein.

QY 421 LIDISSLDATHLGLCDLSTASKHSKPVQEPPLPEVGNINSYMCVEGEAGSKTVLL 480  
 DB 421 lidissldathlglcdl...taskhskp...p...e...vgn... 480  
 OY 481 KKIAITLWASGCCCPPLNRFOLVYVLSSTRPDEGLASICDOLLEKEGSYVEMCNRNIQ 540  
 DB 481 kkiaitlw...asgcccp...lnrfolvylsstrpde...asicdole... 540  
 OS Homo sapiens.  
 XX  
 PN WO9612016-A1.  
 XX  
 PR 25-APR-1996.

QY 541 QLKNOVLFLLDDYKEICSIPOVIGKLIQKHLSLRTCLLAVRNARDIRYLETILEK 600  
 DB 541 qlknqlifl...dykeics...pqv...q...l...k...h...l...a...r...n...a...r...d...i...r...y...l...e...k 600  
 OY 601 AEPFYNNVTCILRKLUSSHMRRLRFEMYFEGKNSLOKTOQTPFLVAAICAHMFQYPDPS 660  
 DB 601 aepf...y...nnv...tc...ilrklu...shmr...rl...rfemyf...eg...k...n...s...l...o...k...t...p...f...l...v...a...a...i...c...a...h...m...f...q...y...p...d...p...s 660  
 OY 661 FDDAVAFKSMERISLRNATAELKATWVSSCGELALKGFFSCCFERNDDLAEAGYDEL 720  
 DB 661 fddavafk...sm...er...i...lr...n...a...t...e...l...k...a...t...w...v...s...c...g...e...l...a...l...k...g...f...s...c...c...f...e...r...n...d...d...l...a...e...a...g...y...d...e...l 720  
 OY 721 EDUTMCLMSKFTQARLPRPFYRELSPAQEFGLGMRLIELLSDROBHQDGLYHKOIS 780  
 DB 721 edutmclmsk...ftqar...lpr...p...f...y...r...e...l...s...p...a...q...e...f...g...l...g...m...r...l...e...l...s...d...r...g...h...g...d...g...l...y...h...k...o...i...s 780  
 OY 781 PMMTVSAYNFNLVYVSSPLSTRAKGPKVSHALVUNKESENTEENDDLKHOPEISQ 840  
 DB 781 pmmtvsaynf...nlv...y...v...s...p...l...s...t...r...a...k...g...p...k...v...s...h...a...l...v...u...n...k...e...s...e...n...t...e...e...n...d...d...l...k...h...o...p...e...i...s...q 840  
 OY 841 MOLRGWMOICPOAYSMSVWSEILVLAULKAYOSWVAACSPVYQFLOGRTLTGAINL 900  
 DB 901 mqjrlrgwqicp...q...y...s...v...m...s...v...e...i...l...v...a...l...k...a...y...s...t...v...a...c...s...p...f...l...q...r...t...l...g...a...i...n...l 900  
 OY 961 ERNLAKEDNVKSYMDMQRASPDLSITGWKLSPQKYKIPCLVCDVNDIDVUGQDMIEL 1020  
 DB 961 ernla...ednvk...sy...md...mqr...a...s...p...d...l...s...i...t...g...w...k...l...s...p...q...k...y...k...i...p...c...l...v...c...d...v...n...d...i...d...v...u...g...q...d...m...i...e...l 1020  
 OY 1021 MTVFSRSORBLHLNHSRGGFESTIRPALELSKASVTYCISKELSNAEQEELLMLPSL 1080  
 DB 1021 mtvfsasqri...l...h...n...h...s...g...f...s...i...p...a...l...s...k...a...s...v...t...c...i...s...k...e...l...s...a...a...e...g...l...i...t...p...s...l 1080  
 OY 1081 SLEVSGTISQDQTPNLDKFLCICKLSVLDLGRNINVSVIPEEFPNHMEKLLIQSA 1140  
 DB 1081 slevsgt...isq...d...q...t...p...n...l...d...k...f...c...i...c...k...l...s...v...d...l...g...n...i...n...v...s...p...e...e...f...p...n...h...m...e...k...l...l...i...q...s...a 1140  
 OY 1141 EYDSKLVLIONSPNLAVPHLICNFNSDRSILMTMVSCKLTERKFSSFFQAVPFWA 1200  
 DB 1141 eydp...sk...v...k...l...i...q...s...p...n...h...f...h...k...c...n...f...s...d...f...s...l...m...t...l...v...s...c...k...t...e...k...f...s...d...f...f...q...a...p...f...w...a 1200  
 OY 1201 SUFNISKILNLLEGQOPDDETSSEFAVYIGLSLNEELILPGDGIRVAKULIQOCQ 1260  
 DB 1201 sufniski...l...n...l...e...g...q...p...d...d...e...t...s...e...f...a...v...y...i...g...l...s...l...n...l...e...e...l...i...l...p...g...d...g...i...r...v...a...k...u...l...i...q...o...c...q 1260  
 OY 1261 QHCLRVLISFKRLNDSSWVIAKV 1285  
 DB 1261 qhclrv...i...s...f...k...r...l...n...d...s...s...w...v...i...a...k...v 1285  
 DE Neuronal apoptosis inhibiting protein.





AAG67527	ID : AAG67527 standard; Protein: 1070 AA.
AC	
XX	
DT	26-NOV-2001 (first entry)
DE	Amino acid sequence of a human secreted polypeptide.
XX	
KW	Human; secreted polypeptide; nervous disease; muscular disease; tumour; gastrointestinal ulceration; spinal cord disease; trachea disease; thyroid gland disease; ovary disease; prostate disease; heart disease; renal gland disease; small intestine disease; thymus disease; lymph node disease; muscular system disease; colon disease; lipase deficiency; cystic fibrosis; pancreatitis; clot formation; myocardial infarction; angioplasty; liver disease; coagulation disorder; microbial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis; vascular smooth cell proliferation; vaccine. Homo sapiens.
CC	
OS	
XX	
PN	W020166690-A2.
PD	13-SEP-2001.
XX	
PP	05-MAR-2001; 2001WO-US07143.
XX	
PR	05-MAR-2000; 2000US-0187107.
PR	13-MAR-2000; 2000US-0188916.
PR	03-OCT-2000; 2000US-0236874.
PR	03-OCT-2000; 2000US-0237846.
PA	(SMIK ) SMITHKLINE BECHAM CORP.
PA	(SMIK ) SMITHKLINE BECHAM PLC.
XX	
PT	Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX	
DR	WPI; 2001-570768/64.
DR	N-PADB; AAH78219.
PS	Claim 1; Page 92-95; 102PP; English.
XX	
PT	Novel isolated secreted polypeptide useful for treating nervous and muscular diseases, gastrointestinal ulceration, coagulation and immune disorders, microbial diseases, inflammation and transplant rejection -
XX	
CC	The present sequence represents a human secreted polypeptide. The secreted polypeptides and polynucleotides are useful for treating nervous and muscular diseases, for inhibiting tumour formation and metastasis, for treating gastrointestinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, ovary, prostate, renal gland, small intestine, heart, trachea, thymus, lymph node, muscular system and colon, for treating lipase deficiency in cystic fibrosis and pancreatitis, for treating undesirable clot formation such as myocardial infarction, during angioplasty and all surgical procedures that require decreased blood clot formation, for treating liver diseases, coagulation disorders and microbial diseases, for treating immune disorders, for treating inflammatory and transplant rejection, for enhancing bone thickness and increasing bone density, for reducing the loss of essential ferroxidases, for suppressing apoptosis, and for regulating vascular smooth cell proliferation. They may also be used as vaccines.
CC	
CC	Sequence 1070 AA;
QY	2 ykslnidecdlhwildpaekplgvnnrv-----cwgfi-rrkgymyp 43
QY	332 LD----DHRCRCPNCPEFLQNMKSSA--EVPPDL----OSRGEL---CPLLETTSES 374
Db	44 ldylnfikdnsra---1lrmqmtvqkqtdldflfwnvnlnrevennickevgeada 98
Db	44 ldylnfikdnsra---1lrmqmtvqkqtdldflfwnvnlnrevennickevgeada 98
QY	375 NLEDLSIAVGPPVPEMAQGEAQMFQEAQNLLNEQRAATSAASFRHMSLIDISLDATD-- 431
Db	99 g1---ihmllkgesescnflksikewnpplfqgngsqfhqsegadldlaqlkd 153
QY	432 -----HLGCGDSI--ASKHSKPV-----OEPPLVAPERVNLSNMCV 468
Db	154 lyhtpsflnfyplgeoididifnlksttpeplwirkdqhhhvqeqltinglqalqspcl 213
QY	469 EGEAASSGKTVLKKKFLWASGCCPLNRFQLEVYSLSSSTRPDEGASICRDOLLKEG 528
Db	214 egeskgkfstilqrmlwgsgkaktkkrkfirs-raqqgfetidcqdlipg 271
QY	529 SYTEMOMRNNTIQQLKQVLFLLDDKWEICSIQ--VIGKLQKHNHSRTCLLAVITNR 585
Db	272 tirkqt-fmamliklqravlfldigynef-kpgncpeiaikenrkfnkmvitttce 329
QY	586 ARDIRYLETILELIKAPPFNVNCUCLKLFNSMTRRKFMYFGKQNSLOKIOKTFEV 645
Db	330 lrhitrqfgaltaevqmgntedsaqalirevilkela--eglliqqnsrcrlnmktlpfv 387
QY	646 AAICAHWFOYFPDPSPFDVDAVFKSYMRSLSNK-----ATAEILKATVSSCGELALK 699
Db	388 vltcaq-qmgeesefhshqtifhtfdql14knkhkgvasdfir-slidcgaleg 446
QY	700 FFSCCFEFNDDDLAEGVDEBDLTCMLMSKTAORLPYREFLSPAFOEFLAGMRLTEL 759
Db	447 vfrskdfelqdv--ssvnedvlitglickytaqrkpkkyffkhsfqeytagrissl 504
QY	760 LDSLREHQDGLYHKIQINSMMTYSAYNNLIVY--SSLPSTKACKPKVSHLHVDN 817
Db	505 ltshepeevtkqngylqkmvsisidstiysslyrtcygssveatra--vmkhlaayqh 561
QY	818 -----KESLENTEENDDYLKHOPESTSQMOLRGLWQICPQAFPSMWEH 862
Db	562 gcllglsiakrplwrslnqsvn-----treqlkl-----ninsfeegih 606
QY	863 LIVLALKTAYGSNT-VAACSPFVLQFLOGRTLTGALNL-QYFFDHPESSLRSIRHPI 920
Db	607 1-----yqestksalsqefafeafqgklyinnsnipdlyf----- 643
QY	921 RGNKTSRRAHSVLSLECEDKSQQPTIDYDSAFEPRINENWEINLAEKEDNUVSYMDMRR 980
Db	644 -----ffehprc--asaldfkldfyyg--amaswe----- 672
QY	981 ASPDLSTGTYWKLUPLSKQKIP-----CLEVDVADIVQGQDMLELMIVFS 1025
Db	673 aaedtgimhseapepy-ipravslfnwqkgeftrtirdfskinkqdriykgfks 731
QY	1026 ASORIEHLNHSRGFTESIRPALESKAVSVTKCSISKELSAEQLLTPLSLEVS 1085
Db	732 satsrlqikrcagwagslsvlstck-niyvslmvaeplrederrhsvrnlktish 790
QY	1086 GTIQSDQDIFEN-LDQFLKLUKELSVLEGNIINVFSVPEEPNPFHMEKLIQISEYD 1143
Db	791 --dqaqqrqrggldslgnknktlimdnlkm----- 825
QY	1144 PSKLVKLULONSPNLHVFHULKONFESDPSGLWMMLVS-----CKKLTEIKFSDSF--QA 1195
Db	826 aiklaegikkkmcmcfhl-thlisdigeyydkvklsepc-dleelqvlscclsana 882

QY 1306 TEGCYRNFFQALDNMPNQEIDISRHTECTIKAQMTVKSISQCVLRPRLIRLNLMSL 1 365  
Db :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 996 ssdgwlatmgvfenlkqvlvdts---tkeflpdpalvrklsvqskltflqearlvqwg 1052  
QY 1366 LADDILL 1 374  
Db 1053 fdddlavi 1061

RESULT 11  
XX AAU02880  
ID AAU02880 standard; Protein; 1024 AA.  
AC AAU02880;  
XX DT 12-SEP-2001 (first entry)

XX DE Human caspase recruitment domain 12 (CARD-12) polypeptide #1.  
XX Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;  
KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;  
KW systemic lupus erythematosis; arthritis; neurological disorder; stroke;  
KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;  
KW aplastic anaemia; myocardial infarction; inflammatory disorder;  
KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;  
KW psoriasis; graft rejection; bacterial infection; leprosy; leprosy;  
KW tuberculosis; ischaemic brain injury; hypoxic brain injury;  
KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
XX excitotoxic brain damage; liver disease.

OS Homo sapiens.  
XX WO20010971-A2.

PD 03-MAY-2001.

XX PR 26-OCT-2000; 2000WO-US29643.

PA (MILLI-) MILLENNIUM PHARM INC.

PL Bertin, J., Robison KE;  
XX DR WPI; 2001 308628/32.  
DR N-PSDB; RAS03945.

PT Isolated caspase recruitment domain-12 polypeptide and nucleic acids  
PT encoding them, useful for treating and diagnosing disorders associated  
XX disease.

XX Claim 9; Fig 1; 93pp; English.

CC The sequence represents a human caspase recruitment domain 12 (CARD-12)  
CC polypeptide. CARD domains are found in a number of proteins that transmit  
CC signals that activate apoptosis and inflammatory pathways in response to  
CC stress and other stimuli. Therefore, CARD-12 and its corresponding  
CC nucleic acid may be used in treatment and diagnosis of patients suffering  
CC from disorders associated with an abnormal level (an increase or a  
CC decrease) of apoptotic cell death or abnormal activity of stress-related  
CC pathways. The disorders include cancer, viral infections (e.g. caused by  
CC poxviruses, adenoviruses), autoimmune disorders (e.g. systemic lupus  
CC erythematosis, arthritis), neurological disorders (e.g. Alzheimer's  
CC disease, amyotrophic lateral sclerosis), haematologic diseases (e.g.  
CC aplastic anaemia, myocardial infarction, stroke), inflammatory and immune  
CC system disorders (e.g. Crohn's disease, insulin-dependent diabetes,  
CC contact dermatitis, psoriasis, graft rejection), bacterial infections  
CC (e.g. tuberculosis, leprosy), ischaemic and hypoxic brain  
CC injury, kidney ischaemia/reperfusion injury, excitotoxic brain damage,  
XX acute bacterial meningitis and liver disease.

SQ Sequence 1024 AA;

Query Match 8.9%; Score 653; DB 22; Length 1024;  
Best Local Similarity 23.7%; Pred. No. 1.9e-45; Indels 238; Gaps 42;  
Matches 263; Conservative 197; Mismatches 410; Index 238; Gaps 42;

QY 344 FLONMKS-SAEVTPLQSLQGELCELETTSESNELEDSIAVGPVTPEMAQGEAQWFEAKN 402  
Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
Db 69 filksikewnwypfqlglnsq---slfhqftsgld----- 100

QY 450 QEPLVLPPEVFGNLSVMQCVGEAGSGKVWLKTAFLWAASCOPLNRFQFVYLSST 509  
Db 149 veqtinglqlaqspcliegesgkgkstlgrianiwgskckaltkfktffirls-- 206  
QY 510 RPDEGLASTICDOLLEKRGGVTEMCMNTIIOQLKNOVLFEDDYKRCISPO--VIGR 566  
Db 207 raggfifetcdqldptgtirkqtfnamlikirkqrifildgynef--kpqncpeiesl 264  
QY 567 IONHILSRKLTAVRNARDIRYLETLEIKAFPVYIVCIRKLFSHHNTRLRKFM 626  
Db 265 ikenhrfknnvmyitltteccirhrgfalgalaevgantedsaqaiarevlikea--egli 322  
QY 627 VVFGKNOSLQKTOKTPFLVAAICAHWFQYFDPSPDDVAVFKSIMERUSLRNK----A 680  
Db 323 19jqksclrlmktpfivwtcafqmgesethstqttlfhydlliqknhkhqva 382  
QY 681 TAELKATVSSCGEALKGKGFSCCFNFDDLAQGVEDDEDLTMCLMSKFTAQRLRPFY 740  
Db 383 asdfir-sldhgdcialegyfrshkrdfeqd--ssvndewlittglickyqeqrkpy 439  
QY 741 RPLSPAFQEFQAGMULIELUDSDQHQDLSKLUKQNSPMATVSYANFNRYV--SSL 798  
Db 440 kfkhksfrqeytagrrrissltsheeveptkgnglyqlqunvsidtslyssllrytcgssv 499  
QY 799 PSTKAGPKVUHHLUVDN-----KESENLESENDDYLLKHOREPISQML 843  
Db 500 eatr---mkmhaavyqigcglqislakrplwrgeslqskn-----:||:||:  
QY 844 LRGLWQICPQAYESWMSHEULLVLALKTAYOSNT-VAACSPFVLOFQLOGRRTUGALNL-Q 901  
Db 546 lkai---ninsfvrcgihl-----ygeatskalsqseafeafqgkqlyinsgnpd 593  
QY 902 YFFHPESLISLRSIHFPIRGKNTSPRAHFSVLETCDPKSVPTQDYSASFEMNE 961  
Db 594 ylfed-----ffahlpnc--asaldfklfdyg--amaswe 625  
QY 962 RNLAEKEDNVSKYMDMORRASDLSGYWKISKPKYKIP-----CLEVDV 1006  
Db 626 -----kaedtgjihmeeqa----- 111  
QY 1007 NDIDVVGODMLETMVFSASQRIELHLNHSRGFLESIRPALELSKASYTKCSISKELS 1066  
Db 667 rctskinkqdtylgkifssatsrlqkragvagslsvlvtck-diyslnveaspit 725  
QY 1067 AAEQELLTTLTSLSELEVSCTIOSDQPN--LDKFLCLKEVSVDLEGNNIWFSVIE 1124  
Db 726 ledernitsvnntktsih---dnqngrqipgfdtsignktk1mdnkm----- 775  
QY 1125 FPNFHMEKLUUOIISAEVPSSKLUKLIQNSPNUVHUKCNFFSDFGSLSMTLV----- 1179  
Db 776 -----needalktaegknkkncklflh---tlstdgegmdyivklsse 818  
QY 1180 -CKKUTETRPSDF---QAVPFWA-SLPNFISIKILNLEGGQFPDEETSEKFAYTIGLS 1235  
Db 819 pcdleelqivscslnsanavkilaqnlhnlvkslidi-senylekognealheilrmn 876  
QY 1236 NLEE---LILPPTGCGIYRVAKLIIQQCQOLRQCLRVISFFKTINDDSVWELAKVATSGCF- 1291



XX			DE	Amino acid sequence of a human secreted polypeptide.
KW	Human; colon cancer; colon cancer antigen; diagnosis; detection;		XX	
KW	identification; cytostatic; cardioactive; neuroprotective; pulmonary;		KW	Human; secreted polypeptide; nervous disease; muscular disease; tumour;
KW	immunomodulatory; muscular; gynaecological; gastrointestinal;		KW	gastrointestinal ulceration; spinal cord disease; trachea disease;
KW	nephrotoxic; antiinfective; antibacterial; gene therapy; wound;		KW	thyroid gland disease; ovary disease; prostate disease; heart disease;
KW	neural disorder; immune system disorder; muscular disorder;		KW	renal gland disease; small intestine disease; thymus disease;
KW	reproductive disorder; gastrointestinal disorder; renal disorder;		KW	lymph node disease; muscular system disease; colon disease;
XX	Infectious disease; cardiovascular disorder.		KW	lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
OS	Homo sapiens.		KW	microbial infection; angioplasty; liver disease; coagulation disorder;
XX			KW	bone thickness; bone density; ferric oxide loss; apoptosis;
PN	W020055351-A1.		KW	vascular smooth cell proliferation; vaccine.
XX			XX	
PD	21-SEP-2000.		XX	
XX			XX	
PF	08-MAR-2000; 2000WO-US05883.		XX	
XX			XX	
PR	12-MAR-1999; 99US-0124270.		XX	
XX			XX	
PA	(HUMAN-) HUMAN GENOME SCI INC.		XX	
XX			XX	
PI	Rosen CA, Ruben SM;		XX	
XX			XX	
DR	WPI; 2000-587534/55.		XX	
DR	N-PSDB; AAC98250.		XX	
PT	Colon cancer associated gene sequences, referred to as colon cancer		XX	
PT	antigens, useful for the treatment, prevention, and diagnosis of colon		XX	
XX	disorders such as colon cancer -		XX	
PS	Claim 11; Page 1612; 2104pp; English.		XX	
CC	AAC97991 to AAC98763 encode the human colon cancer associated proteins,		XX	
CC	called human colon cancer antigens, given in AAB51234 to AAB54006. The		XX	
CC	human colon cancer antigens can have cytostatic, cardioactive, muscular,		XX	
CC	neuroprotective, immunomodulatory, gynaecological, gastrointestinal,		XX	
CC	vulgar, nephrotoxic, antiinfective and antibacterial activities, and		XX	
CC	can be used in gene therapy. The colon cancer antigen polynucleotides, and		XX	
CC	proteins and antibodies to the proteins are useful for the prevention,		XX	
CC	treatment and diagnosis of colon disorders, such as colon cancer. The		XX	
CC	polynucleotides may be used in diagnostics and research, such as for		XX	
CC	chromosome identification, and as hybridisation probes. The proteins		XX	
CC	may also be used to prevent diseases such as neural disorders, immune		XX	
CC	system disorders, muscular disorders, reproductive disorders,		XX	
CC	diseases, and cardiovascular disorders. AAC98764 to AAC98772 and		XX	
CC	AAB54007 represent sequences used in the exemplification of the present		XX	
CC	invention.		XX	
Sequence	118 AA;		XX	
Query Match	7.5%;	Score 545.5;	DB 21;	Length 118;
Best Local Similarity	95.5%;	Pred. No. 6.4e-38;	Matches 106;	Conservative 1;
Mismatches	1;	Indels 3;	Indels 1;	Gaps 1;
OY	607	TVCILRKLFSHNNTTRLRFMVMVFGKNSQLOIQLPFLVAICAWFQPPDFSDDVAV	666	
Db	1	tvcilrklfshnnttrlrfmvmvfgknsqloiqlpflvaicawfqpdpdfddav	60	
OY	667	FKSIMERLSSLRNKATABELKAVVSSGELAKGFFSCCTEFND-DDLAEG	716	
Db	61	fksimerlsslrnkataelkavvssgelakgffscctefnd-ddlaeg	111	
RESULT	14			
AAG67526				
ID	AAG67526 standard; Protein; 738 AA.			
XX				
AC	AAG67526;			
XX				
DT	26-NOV-2001 (first entry)			
QY	344 FLOMKS-SAETPDQSRGECELEUTSESSNLEDIAVGPVPEMAQEWQEAKN	402		
Db	55 fksimerlsslrnkataelkavvssgelakgffscctefnd-ddlaeg			
QY	403 LMEQLRAAYTSAFRMSLUDISSLATELJGCDLSI--ASKHISKPV-----	86		
Db	87 laqdldlyhtpsinf-----ypgedidifnlkstrieplwrdqhhhr	449		
QY	450 QPVLVLPVEVFGNLNSVMCVEGEAGSGKTVLRLKIAFLWASGCCPLINRFDIVYKLSSEN	509		

Db 135 vegtlngilqalqspciegesgkqkstlqriamlwgsgkckaltkfkffrls-- 192  
 XX PN WO9723501-A1.  
 QY 510 RPDGEGLASICDQOLEKEGGSVTMCMRNITQQQLKNOVLEFLDDYKEICSIPO--VIGKL 566  
 XX PD 03-JUL-1997.  
 Db 193 raaggflfetlcqdldipatirkrtfmamllkqrvflldgynef--kpqncpeieal 250  
 XX PR 20-DEC-1996; 96WO-AU00827.  
 QY 567 IOKNHLSRCLLLIAVRTRNRARDIRYLETLEKAFPFVNTVCILRKLFSHNMWRLRKF 626  
 XX PR 22-DEC-1995; 95AU-0007275.  
 Db 251 1kenhrfknnvvitltteclrhqfaltaevgdmtedasaqaalirevikela--egli 308  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 XX PR  
 QY 627 VFGGINOSIQIOKUPFLYAAICAIWFQPPFDPSFDDWAVFKSMEWLRSBNK-----A 680  
 PI vaux DL;  
 XX DR  
 Db 309 lqiqksrcirnlmktpifvvitca1qmgeasefhstqtltifhfydliqknkhkgva 368  
 DR N-PSDB; AAT72711.  
 QY 681 TAEIKATVSSCGELALKGFCCPEFNDDLAEGVDEDEDLTMCLMSKFTORLRPFY 740  
 XX PT Isolated protein homologues of viral inhibitors of apoptosis - used  
 Db 369 asdfir-sdbcgialdavlyfshsfafelqdy--ssvnedvlitglickytaorfkpy 425  
 PT to modulate apoptosis for treatment of degenerative, infectious or  
 QY 741 RFLSPAFQETFLAGMPLIELUDSDRQEHDQDGLLYHUKQINSPMMTVASYANFLNYV--SSL 798  
 XX PT autoimmune diseases and cancer.  
 Db 426 kfhhksfqeytagrlsltshepeavtkgnqylqkmvisidtstyssllrytcgssy 485  
 PS Claim 8; Page 51-54; 136pp; English.  
 QY 799 PSTKAGPKVIVSHLHLWDN-----RESLENISENDDYLHQPELSLOMOL 843  
 CC Mammalian IAP homologue B (MIHB) (AAW19746) is a human homologue of  
 CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid  
 sequence was deduced from a cDNA clone (see also AAT72711) isolated  
 CC from a human foetal liver cDNA library using primers based on  
 CC human EST sequences that resembled the BIR repeats of Oryzias  
 CC pseudotsugata polyhedrosis virus IAP. IAP homologues (see also  
 AAW19745 and AAW19747-52) and their derivatives and chemical analogues  
 CC can be used in methods for modulating apoptosis in animal cells,  
 CC specifically for treatment, by inhibition, of degenerative and  
 CC infectious disease or, by promotion, of cancer and autoimmune  
 CC disease.  
 XX SQ Sequence 618 AA:  
 Db 612 -----kaedtggiimeapepy-ipsravslffnwqkgeftrlevtl 652  
 QY 1007 NDIDVGQDMILELUMTVFSASQRIELHLNHSRGFIESIRPAELSKASVYKCSISKELES 1066  
 Db 653 rdfsdklinkdiryqkifssatsrslrqikraqagslsvistck-niyimveaspit 711  
 QY 1067 AAEQELLLTIPSLESLIEVSGTIQSQ 1091  
 Db 712 iederhitsvnktlsih-dlqnq 735  
 RESULT 15  
 AAW19746  
 ID AAW19746 standard; Protein; 618 AA.  
 XX AC AAW19746;  
 AC AAW19746;  
 DT 16-SEP-1997 (first entry)  
 DE Human inhibitor of apoptosis protein homologue MIHB.  
 XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHB;  
 KW degenerative disease; infectious disease; autoimmune disease;  
 KW cancer; therapy; diagnosis.  
 KW Homo sapiens.

**Key Location/Qualifiers**

FT Region 46..113  
 FT Region /label= BIR 184..250  
 FT Region /label= BIR 269..337  
 FT Region /label= BIR 569..606  
 FT Region /label= RING\_finger

Query Match 6,3%; Score 462; DB 18; Length 618;  
 Best Local Similarity 26.0%; Pred. No. 1.1e-29; Matches 155; Conservative 82; Mismatches 214; Gaps 22;  
 Matches 155; Conservative 82; Mismatches 214; Gaps 22;  
 Db 38 LEEEFQEKARAKMQKYNNSHRSEAKRLKRTVYEEYSSWIP--QEMAJAGFYFTGVKG 94  
 QY 95 IQFCGCSLILFGAGTRLPEDHKRFHDFG---LINKDGVNTAKYDVRKN----- 144  
 Db 81 vkcfcggmlndnwkgdsp1qkhkjlypescfpiplvslsglsksntsppmrnfahsis 140  
 QY 145 -----LKSRL-----RGKMRY--QEEFARLASFRNNPFYVOG 175  
 Db 141 ptlehsslfgsyssllspnplsnavedissrrtpysamstearlfhyamp--lf 198  
 QY 176 ISPVCVISEAGVFTKQDPTVOCESGGCGLNWECDPPEHEAKWPKREFLRSKSS 235  
 Db 199 lpselaragiyigpdravfacfcgk1snwepkdamssehrhrfpncptl--ensie 255  
 QY 236 ITQYIOSKKGFDVDTGEHENFNSWQRELPMAASAYCNDSFAVEEURLDSEKDWRPESAVG 295  
 Db 256 trfsls-----nlsinqt-----haarmtmywswsvprq 286  
 QY 296 VAALAKAGLFTGIKDIVOFSCGGCLEKKWQEGDPLDPRTRCFANCPLQNMKSSAETV 355  
 Db 287 peqlasagfyygradvckccdg91rcwesgadpwhakwfprcef1rmqg-efv 345  
 QY 356 PDLQR-GECELLENTSESNLEDSTAVGPVPEMAQGEAOFWOEAKNINEOLRAYTS 414  
 Db 346 deiqgryphileglisstdtgeen--adppihfgpess-sedavmuntpvksalem 402  
 QY 415 SFRHMSLDISSLATDHLUGCDLSIASKISKPVQEP-LVLPYEVGNINSVMCGVEG 473  
 Db 403 qfnr-----dl----vktvqsklittgnyktrndivaline 438

OY 474 SCKTVLIK-KIAFLWASGCCPLNREPOLVFVLSSTRDEGLASTICDOLLEKGSVTE 532  
Db 439 dekreeekqaeemadsdislirknrmalfqqtcvlp-----ilgnlk----- 484  
OY 533 MCMRNNTIOQLNQVLQTLDYKEICSIPOVIGKLITQKNHLSRTCLLIAVRTNRARDI 589  
Db 485 --anvinkqehdi-----kqktqiplqareld-----tilvkgnnaani 523

Search completed: September 30, 2002, 15:04:43  
Job time: 324 sec

Run on: September 30, 2002, 15:00:54 ; Search time 19.98 Seconds  
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OM protein - protein search, using sw model

Run on:	September 30, 2002, 15:00:54 ; Search time 19.98 Seconds				
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Perfect score:	7308				
Sequence:	1 MATQQKASDERISQFDHNL.....SKYLTILQKWLWLFSPITQK 1403				
Scoring table:	BLOSUM62				
Gapop:	10.0 , Gapext: 0.5				
Searched:	231628 seqs, 2442594 residues				
Total number of hits satisfying chosen parameters:	231628				
Minimum DB seq length:	0 (without alignments)				
Maximum DB seq length:	200000000				
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries				
Database :	Issued_Patents_AA:*				
1:	/cgn2_6/podata/2/iaa/5A_COMB.pep:*				
2:	/cgn2_6/podata/2/iaa/5B_COMB.pep:*				
3:	/cgn2_6/podata/2/iaa/6A_COMB.pep:*				
4:	/cgn2_6/podata/2/iaa/6B_COMB.pep:*				
5:	/cgn2_6/podata/2/iaa/PCTUS_COMB.pep:*				
6:	/cgn2_6/podata/2/iaa/backfile1.pep:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query Length	DB ID	Description	
1	6373.5	87.2	1232	3 US-08-036-134-2	Sequence 2, Appl
2	5955	81.5	1151	3 US-08-036-134-23	Sequence 23, Appl
3	462	6.3	18	2 US-08-511-485-8	Sequence 8, Appl
4	462	6.3	618	3 US-09-212-971-8	Sequence 8, Appl
5	462	6.3	618	4 US-09-050-929A-8	Sequence 8, Appl
6	462	6.3	618	4 US-08-059-749-2	Sequence 2, Appl
7	462	6.3	618	4 US-09-517-053A-8	Sequence 8, Appl
8	462	6.3	618	4 US-09-059-023-29	Sequence 29, Appl
9	462	6.3	618	5 PCT-US61-12860-2	Sequence 2, Appl
10	457.5	6.3	612	3 US-09-212-971-14	Sequence 14, Appl
11	457.5	6.3	612	4 US-09-050-929A-14	Sequence 14, Appl
12	457.5	6.3	612	4 US-08-059-749-14	Sequence 14, Appl
13	457.5	6.3	612	4 US-09-517-053A-14	Sequence 14, Appl
14	457.5	6.3	612	5 PCT-US61-12860-14	Sequence 14, Appl
15	440	6.0	600	3 US-09-212-971-12	Sequence 12, Appl
16	440	6.0	600	4 US-08-050-929A-12	Sequence 12, Appl
17	440	6.0	600	4 US-09-517-053A-12	Sequence 12, Appl
18	437.5	6.0	496	2 US-08-511-485-10	Sequence 10, Appl
19	437.5	6.0	496	3 US-09-212-971-10	Sequence 10, Appl
20	437.5	6.0	496	4 US-08-050-929A-10	Sequence 10, Appl
21	437.5	6.0	496	4 US-09-517-053A-10	Sequence 10, Appl
22	436.5	6.0	604	4 US-08-059-749-4	Sequence 4, Appl
23	436.5	6.0	604	5 PCT-US96-12860-4	Sequence 4, Appl
24	431.5	5.9	604	5 US-08-059-485-6	Sequence 6, Appl
25	431.5	5.9	604	3 US-09-212-971-6	Sequence 6, Appl
26	431.5	5.9	604	4 US-08-050-929A-6	Sequence 6, Appl
27	431.5	5.9	604	4 US-07-177-032A-6	Sequence 6, Appl

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0 (without alignments)  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database :

- 1: Issued\_Patents\_AA:\*
- 2: /cgn2\_6/podata/2/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/podata/2/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/podata/2/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/podata/2/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/podata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**ALIGNMENTS**

RESULT 1  
 US-08-036-134-2

; Sequence 2, Application US/08836134A  
 ; patient No. 6020127  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mackenzie, Alex E.  
 ; APPLICANT: Korneluk, Robert G.  
 ; APPLICANT: McLean, Michael  
 ; APPLICANT: Roy, Natalie  
 ; APPLICANT: Ikeda, John E.  
 ; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene sequence and  
 ; Patent No. 6020127  
 ; TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy  
 ; FILE REFERENCE: 3477-112, 033477-139914  
 ; CURRENT APPLICATION NUMBER: US/08-0836,134A  
 ; CURRENT FILING DATE: 1997-06-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 1232  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-08-0836-134-2

Query Match 87.2% ; Score 6373.5 ; DB 3 ; Length 1232;  
 Best Local Similarity 95.9% ; Pred. No. : 1; Mismatches 1; Indels 51; Gaps 1;

Matches 1229; Conservative

QY 1 MATQQKASDERISQFDHNLPELPSALLGDAVOLAKELBEEQERAKMQKGYNQSMRSE 60  
 |||||||KKKQKASDERISQFDHNLPELPSALLGDAVOLAKELBEEQERAKMQKGYNQSMRSE 60  
 Db 1 MATQQKASDERISQFDHNLPELPSALLGDAVOLAKELBEEQERAKMQKGYNQSMRSE 60  
 |||||||KKKQKASDERISQFDHNLPELPSALLGDAVOLAKELBEEQERAKMQKGYNQSMRSE 60  
 QY 61 AKRLKTFVTVYEPYSSWIPQDMAAGPYFTCQVKSGIQFCFCSLTLFGAGLTLRPLDHKRF 120  
 |||||||KKKQKASDERISQFDHNLPELPSALLGDAVOLAKELBEEQERAKMQKGYNQSMRSE 60  
 Db 61 AKRLKTFVTVYEPYSSWIPQDMAAGPYFTCQVKSGIQFCFCSLTLFGAGLTLRPLDHKRF 120  
 |||||||KKKQKASDERISQFDHNLPELPSALLGDAVOLAKELBEEQERAKMQKGYNQSMRSE 60  
 QY 181 LSEAGGVFTGKQDTWCFSGGGCLGNWEEQDDPWRKPKWPKFKEFLRSKSSEITQYI 240  
 |||||||KKKQKASDERISQFDHNLPELPSALLGDAVOLAKELBEEQERAKMQKGYNQSMRSE 60  
 Db 181 LSEAGGVFTGKQDTWCFSGGGCLGNWEEQDDPWRKPKWPKFKEFLRSKSSEITQYI 240  
 |||||||KKKQKASDERISQFDHNLPELPSALLGDAVOLAKELBEEQERAKMQKGYNQSMRSE 60  
 QY 241 OSYKGFVDITGEHFWNSWORELPMASAYCNDSITAYEELRLDSFKDWPRESAVYALA 300  
 |||||||KKKQKASDERISQFDHNLPELPSALLGDAVOLAKELBEEQERAKMQKGYNQSMRSE 60  
 Db 241 OSYKGFVDITGEHFWNSWORELPMASAYCNDSITAYEELRLDSFKDWPRESAVYALA 300  
 |||||||KKKQKASDERISQFDHNLPELPSALLGDAVOLAKELBEEQERAKMQKGYNQSMRSE 60

**QY** 301 KAGLFYTGIKDVOFCSCGGLEKMQEGDDPLDHTRCFPNCFLQMKSSAVENTPDQS 360  
**Db** 301 KAGLFYTGIKDVOFCSCGGLERKMQEGDDPLDHTRCFPNCFLQMKSSAVENTPDQS  
**QY** 361 RGEELCELLETTSESNLEDSTAVGPVTPENAOEQAQFQEARLNLSNQLRAYTSAFRMS 420  
**Db** 361 RGEELCELLETTSESNLEDSTAVGPVTPENAOEQAQFQEARLNLSNQLRAYTSAFRMS 420  
**QY** 421 LUDTSDDATDHLGCGDSIASKHISKPVQPLVPEVFQNLNSMCVEGEGASGKVLL 420  
**Db** 421 LUDTSDDATDHLGCGDSIASKHISKPVQPLVPEVFQNLNSMCVEGEGASGKVLL 420  
**QY** 481 KTKAFLWASGCCPLNRLQFVLSSTRPDEGLASTICDQOLKEGSVTENCMRNIQ 480  
**Db** 481 KTKAFLWASGCCPLNRLQFVLSSTRPDEGLASTICDQOLKEGSVTENCMRNIQ 480  
**QY** 541 QLKNQVFLFLDYYKECSIPQVIGLQKQHNLRTCLIAVTNRARDIRYLETIEK 600  
**Db** 541 QLKNQVFLFLDYYKECSIPQVIGLQKQHNLRTCLIAVTNRARDIRYLETIEK 600  
**QY** 601 AEPFYNTVCTLRKLFSHNTRLRKFMYFGKNSLOKIQPKLVAICAHWFOPFDP 660  
**Db** 601 AEPFYNTVCTLRKLFSHNTRLRKFMYFGKNSLOKIQPKLVAICAHWFOPFDP 660  
**QY** 661 FDDVAFKSIMERLSTRKATABILKATVSSCGELALKGIFSCFEEFNUDDAEAGVED 720  
**Db** 661 FDDVAFKSIMERLSTRKATABILKATVSSCGELALKGIFSCFEEFNUDDAEAGVED 720  
**QY** 721 EDUTMCLMSKETAQRURPFYRPLSPAFOERLAGMLIELDSRQERODGLYHLQINS 780  
**Db** 721 EDUTMCLMSKETAQRURPFYRPLSPAFOERLAGMLIELDSRQERODGLYHLQINS 780  
**QY** 781 PMMVSYANFNLYVSLPLSTKAGERIVSHLHVDNKESLENISENDWLHKHPEISLQ 840  
**Db** 781 PMMVSYANFNLYVSLPLSTKAGERIVSHLHVDNKESLENISENDWLHKHPEISLQ 840  
**QY** 841 MOLLRGWQOCPOAVSMUSEHLLVLAALKTAYQNTVTAACSFVUOFLQGRTLTGALNL 900  
**Db** 841 MOLLRGWQOCPOAVSMUSEHLLVLAALKTAYQNTVTAACSFVUOFLQGRTLTGALNL 900  
**QY** 901 QYFFDHPESLSSLRSHPRGKNTSRPALESKSYTCISKELSAEQLLUTPSLE 960  
**Db** 901 QYFFDHPESLSSLRSHPRGKNTSRPALESKSYTCISKELSAEQLLUTPSLE 960  
**QY** 961 ERNLAEKEDNVSYMDMORRASPDUSTGYRKSPHQYKPCLEVNDIDVVGQDMILEL 1020  
**Db** 961 ERNLAEKEDNVSYMDMORRASPDUSTGYRKSPHQYKPCLEVNDIDVVGQDMILEL 1020  
**QY** 1021 MTFVPSASQRIELHNLHSRGTESTRPALESKSYTCISKELSAEQLLUTPSLE 1080  
**Db** 1021 MTFVPSASQRIELHNLHSRGTESTRPALESKSYTCISKELSAEQLLUTPSLE 1080  
**QY** 1081 SLEVSQTIQSOQFPNPKFLCKLKSVDLJRCNTNFVSPVPEPNFHMEKLIQISA 1140  
**Db** 1081 SLEVSQTIQSOQFPNPKFLCKLKSVDLJRCNTNFVSPVPEPNFHMEKLIQISA 1140  
**QY** 1141 BYDPKRLVLLIONSPNLPVPHKCNFFSDGSLMTPLVSKKLEIKAISDSFQAVPVA 1200  
**Db** 1141 BYDPKRLVLLIONSPNLPVPHKCNFFSDGSLMTPLVSKKLEIKAISDSFQAVPVA 1200  
**QY** 1201 SLPNFTISLKLNLLEGQDPDETSERFAYLGLSISNLLELILPTDGCIYRVALLIQOCQ 1260  
**Db** 1150 SLMNFIKLNLLEGQDPDETSERFAYLGLSISNLLELILPTDGCIYRVALLIQOCQ 1260  
**QY** 1261 QLKNQVFLFLDYYKECSIPQVIGLQKQHNLRTCLIAVTNRARDIRYLETIEK 129  
**Db** 1210 QLKNQVFLFLDYYKECSIPQVIGLQKQHNLRTCLIAVTNRARDIRYLETIEK 129  
**RESULT** 2  
**US-09-830-338-1.rai**  
**; Sequence 23 , Application US/08836134A**  
**; Patient No. 6020127**

Query Match 6.3%; Score 462; DB 2; Length 618;  
 STRANDBNESS: not relevant  
 TOPOGY: both  
 MOLECULE TYPE: protein  
 US-08-511-485-8

RESULT 3  
 US-08-511-485-8 Application US/08511485  
 Patent No. 5919912

GENERAL INFORMATION:  
 APPLICANT: Korneluk, Robert G.  
 APPLICANT: Mackenzie, Alexander E.  
 APPLICANT: Baird, Stephen

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
 PROBES, AND DETECTION METHODS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/511,485  
 FILING DATE: 04-AUG-1995  
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE DOCKET NUMBER: 07540/002001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 8:  
 SUBSEQUENCE CHARACTERISTICS:  
 LENGTH: 618 amino acids  
 TYPE: amino acid

RESULT 4  
 US-09-212-971-8  
 Sequence 8, Application US/09212971B  
 Patent No. 6107041

GENERAL INFORMATION:  
 APPLICANT: Korneluk, Robert G.  
 APPLICANT: Mackenzie, Alexander E.  
 APPLICANT: Liston, Peter  
 APPLICANT: Baird, Stephen  
 APPLICANT: Teng, Benjamin K  
 APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
 TITLE OF INVENTION: IAP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
 DISEASE

FILE REFERENCE: 07831/000202  
 CURRENT APPLICATION NUMBER: US/09/212,971B  
 CURRENT FILING DATE: 1998-12-16  
 EARLIER APPLICATION NUMBER: 60/0017,354

Query Match 6.3%; Score 462; DB 2; Length 618;  
 Best local Similarity 24.7%; Pred. No. 2.1e-33;  
 Matches 159; Conservative 93; Mismatches 238; Indels 154; Gaps 24

QY 38 LEPEBEOKERAKMOKRGYNSMRSEKRLKFWTYPPYSSNP--OEMAJAGFYFTGVKG 94  
 Db 28 LSDWTNSNKKRMDFSC-----LYKNTYSTFPAGVPVSRSLARAGFYFTGVNDR 80

QY 95 IOCFCCSUJLFGAGGLTRUPIEDHKKRFHPDG --LLNKDVGNTAKYDVRKN----- 144  
 Db 81 VKCFCGGLMLDNWPLGDSPIOKHQLYPRSCFSTNLVSASLGTSKNTSPMRNSFAHLS 140

QY 145 -----LKS-----RGKMRV--QEEARLSPRNTPYVOG 175  
 Db 141 PTLEHSSLFGSWSLSPPNPLNSRAVEDISSRRNPYSTMSTEARFLYHMP--LTF 198

QY 176 ISPCVULSEAGFVTGKGQDVTGOCFSCGGCGLGNWECDPWRKEAHAWPKCEBLRSKSEE 235  
 Db 199 LSPELALAGFYIIGPDRVACFAGGKLSNWPKDDAMSEHRHNPNGPFL--ENSE 255

QY 236 IROYIQSYKGFDUTIGEHEVNWMORELMSAVCNDSTFAYEURLDERFKDWRESAVG 295  
 Db 256 TURFSIS-----NISMOT-----HARMRTPYMWSSPVQ 286

Qy 296 VAIKAKLAFYETIKDINOFCSCGCLERKQEGDPDLHTRCPNCPLQNMMAEV 355  
 Db 287 PEOLASAGRYYVGRNDYKCFGCGDGLRQWESGDPPWHAKWPCEFLTRMGQ-EFY 345

QY 356 PDQGSR-GELCELETTESNLEDIASIAVGPVPIVPMQGAQWFOEAKNLNEQLRAYTA 414  
 Db 346 DEFGQYRPHILEQDUDSTGTGEEN--ADPPTINGPGESS--SDAVMTNPVSALEM 402

QY 415 SF-----REHMUDISDSL-----ATBHLLGDSLSTAS 442  
 Db 403 GFNRDLVKQTIVLUSKLTGENDYKTVNDIVSALLADEKREEREKOAEEMASDDSLIR 462

QY 443 KHISKPYQEPVLVEPEVGH-----NSVMCEGEAGSGKTVL--LKKIAFLWAG----- 490  
 Db 463 KNRMALFOQLTCVLPILDNLLKVNKOEHDTIKQTOIPQLQRELIDTIWIGNAAN 522

QY 491 ---CCPLNRFOLVYFLSSR---PDEGLASITCQOLLEK--EGSVTECMRNII 539  
 Db 523 IFKNC--LKEIDSTLYKLNFKVNKNYKLVPTDLSLSEQRQLEERTCKYCMDKEV 579

QY 540 QQLKNQVFLDGYKECISIPOVTKLQKNHSLTCLLIAVRT 583  
 Db 580 ---SVVFIPCGHLWVC--QECAPSLRKCPICRGIIKTVRT 615

; EARLIER FILING DATE: 1996-04-26  
; EARLIER APPLICATION NUMBER: 60/030, 590  
; EARLIER FILING DATE: 1996-11-14  
; EARLIER APPLICATION NUMBER: 08/800, 929  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO: 8  
; LENGTH: 618  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-212-971-8

## Query Match

Best Local Similarity 6.3%; Score 462; DB 3; Length 618;  
 Matches 159; Conservative 93; Mismatches 238; Indels 154; Gaps 24;  
 Qy 38 LEEBEEQERAKMOKGKYNQNSMRSEAKRLKTVYEPYSSWP--QEMAAAGFYFTGKSG 94  
 Db 2B LSDWTNSNKRKMKYDFDSC--LYRMSYSTTPAGPVPSERSLARAGFYVTGVNDK 80  
 Qy 95 IOPCCSLLIFGAGIUTRPLP-EDHKRFHPCGF--LINKDGNIYAKDVRKN----- 144  
 Db 81 VKCFCGCCGILMDNWKLGDSPIQKHOLYPSFQNLPSFIQNLVSA-SLGSTS 144  
 Qy 145 -----LKSLR-----RGGMRY--QEEEARLASFRNWFYVQ 140  
 Db 141 PTLEHSSLFGSSYSSLPNPNLSRAVEDISSRTTPSYAMSTEARFLTYHMP--LTF 198  
 Qy 176 ISCPVULSEAGFVFTGKQDFTOCFSCGGCLGNWEGDDPKHEAKWFPKCEERSKSSEE 235  
 Db 199 LSPSELARAKAGFYTGPDRVACFACGGKLSNWEPAKWFPEHAKWFPKCEERSKSSEE 235  
 Qy 236 ITQYIOSYKGFVDITGEHFVNWSWORELPMASAYCNDSIFAYEELRUDSFKDWPRESAVG 295  
 Db 255 TLRFSIS-----NLSMOT-----HAARMRPFMWFYVQ 295  
 Qy 286 VAAKAGLFYTGKDIYQCCGCGCCKWQGDPDTRCPNCPCFLQNKNSAETV 286  
 Db 287 PEQLASAGFYIVGRNDVKCFCGDCGGURCWCSSGDDPWVEAHKWFPRCEFLIRMKQO-EFV 355  
 Qy 356 PDLSR-GELC-BLETTSESNLDSIAVGPIVEMQAQGAQWFOAKNINQELRAYTSA 414  
 Db 346 DEICQYRPHLLEOLSLSDTGCEN--ADPPIHFGPGESS-SEDATMNPVVALEM 402  
 Qy 415 SF-----RHMSLUDISDL-----ATDHILGDSLSTAS 442  
 Db 403 GENRDLYKQTWLSKILTGENYKTNIDIVSALLNADEKEEKEKQAEIMASDLSLIR 462  
 Qy 443 KHMSPKVOEPLVLPVFEGNL--NSVMCGVEAGASCKTVI--LKKIAFLWASG---- 490  
 Db 463 KRMALFOQQLTCVAPILDNKLANKVQHQDIIKORTQPLQARELDTIWKGNAAN 522  
 Qy 491 --CCPLNRFQLOVYFLSSTR---PDEGASATICDOLIKK-EGSVTEMCHRNII 539  
 Db 523 IFKNG--LKEIISTSLYKLNFLFDKNNKYITTEDSGLSLSEQRLRQEBERTKVKMDKEV 579  
 Qy 540 QDKNQVFLDQDYKECSTIPQVICKLIONHSLSRCTLLIAVRT 583  
 Db 580 -----SVWFPCGGHLWVC--OECAPSRLRKCPICRGTIKGTVRT 615  
 RESULT 5  
 US-08-800-929A-B

Sequence 8, Application US/0800929A  
 Patent No. 6133437  
 GENERAL INFORMATION:  
 APPLICANT: Korneluk, Robert G  
 APPLICANT: Mackenzie, Alexander E  
 APPLICANT: Liston, Peter  
 APPLICANT: Baird, Stephen  
 APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine  
 TITLE OF INVENTION: DIETECTIVE  
 TREATMENT OF PROLIFERATING  
 DISEASE AND NAP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATING  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Clark & Elbing LLP  
 STREET: 176 Federal Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110  
 COMPUTER READABLE FORM:  
 MEDIUM: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: PastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/800, 929A  
 FILING DATE: 13-FEB-1997  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/030, 590  
 FILING DATE: 14-NOV-1996  
 APPLICATION NUMBER: 60/017, 354  
 FILING DATE: 26-APR-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bleker-Birdy, Kristina  
 REGISTRATION NUMBER:  
 REFERENCE/DOCKET NUMBER: 07891/009001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-428-0200  
 TELEX: 617-428-7045  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 618 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-800-929A-8

## Query Match

Best Local Similarity 6.3%; Score 462; DB 4; Length 618;  
 Matches 159; Conservative 93; Mismatches 238; Indels 154; Gaps 24;  
 Qy 38 LEEBEEQERAKMOKGKYNQNSMRSEAKRLKTVYEPYSSWP--QEMAAAGFYFTGKSG 94  
 Db 2B LSDWTNSNKRKMKYDFDSC--LYRMSYSTTPAGPVPSERSLARAGFYVTGVNDK 80  
 Qy 95 IOPCCSLLIFGAGIUTRPLP-EDHKRFHPCGF--LINKDGNIYAKDVRKN----- 144  
 Db 81 VKCFCGCCGILMDNWKLGDSPIQKHOLYPSFQNLPSFIQNLVSA-SLGSTS 144  
 Qy 145 -----LKSLR-----RGGMRY--QEEEARLASFRNWFYVQ 140  
 Db 141 PTLEHSSLFGSSYSSLPNPNLSRAVEDISSRTTPSYAMSTEARFLTYHMP--LTF 198  
 Qy 176 ISCPVULSEAGFVFTGKQDFTOCFSCGGCLGNWEGDDPKHEAKWFPKCEERSKSSEE 235  
 Db 199 LSPSELARAKAGFYTGPDRVACFACGGKLSNWEPAKWFPEHAKWFPRCEFLIRMKQO-EFV 355  
 Qy 236 ITQYIOSYKGFVDITGEHFVNWSWORELPMASAYCNDSIFAYEELRUDSFKDWPRESAVG 295  
 Db 255 TLRFSIS-----NLSMOT-----HAARMRPFMWFYVQ 295  
 Qy 296 VAAKAGLFYTGKDIYQCCGCGCCKWQGDPDTRCPNCPCFLQNKNSAETV 286  
 Db 287 PEQLASAGFYIVGRNDVKCFCGDCGGURCWCSSGDDPWVEAHKWFPRCEFLIRMKQO-EFV 355  
 Qy 356 PDLSR-GELC-BLETTSESNLDSIAVGPIVEMQAQGAQWFOAKNINQELRAYTSA 414

DB ::::::::::::::::::::: 346 DEIOPGRYPHILEQILQJSTSDTGEEN - ADDPITHFGCSESS - SEDAVIMNTPVVSALEM 402

QY ::::::::::::::::::::: 145 -----LKSRL -----RGKMKY -- QFEEARLASFRNMPPFWQG 175

Db 415 SF-----RUMSLDIDISDI----- -RUMSLDIDISDI----- -ATDHLGCDUSIAS 442

Db 403 GFNRDLVKQTVLSKILTGTGENYTKVNDSALLNAEDEKEREEKEKOAEEMASDDLSLR 462

QY ::::::::::::::::::::: 443 KHISKPVQEPVLPREVFGNL -- NSVACVEGAGSGCTVL -- LKIAFLWASG 490

Db 463 KURMALFQLTCVLPJUDNLLKANVJNKQEHDIKQRTQIPLQARELDTIWVGNAAAN 522

QY ::::::::::::::::::::: 491 ---CCPLINRFOLVFYLSSSTR -- PDEGLASTICDOLLEK - EGSYTEMCRNII 539

Db 523 IFKNC -- LKEIDSTLKLNFDRKNNMRYIPTDVSGLSLEQERLQOERTCKVCMDEV 579

QY ::::::::::::::::::::: 540 QOLKNQVLFLLDYKECSIPQVIGKLUOKNHLRSRCLLIAVRT 583

Db 580 ----SVTEPCGHLWVC -- QECAPSLSRKCPICRGTIKGTVRT 615

RESULT 6 US-08-569-749-2

; Sequence 2, Application US/08569749

; GENERAL INFORMATION:

; APPLICANT: Rotthe, Mike

; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FLEHR, HOHACH, TEST, ALBRITTON & HERBERT

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/569, 749

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Brezner, David J.

; REGISTRATION NUMBER: 24,774

; REFERENCE/DOCKET NUMBER: A-62464/PJB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415)781-1989

; TELEFAX: (415)398-3249

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 618 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Protein

; US-08-569-749-2

RESULT 7 US-09-617-053A-8

; Sequence 8, Application US/09617053A

; Patent No. 63100492

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E

; APPLICANT: Liston, Peter

; APPLICANT: Baird, Stephen

; APPLICANT: Tsang, Benjamin K

; APPLICANT: Pratt, Christine

; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND

; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

; TITLE OF INVENTION: DISEASE

; FILE REFERENCE: 07891/1009003

; CURRENT APPLICATION NUMBER: US/09/617, 053A

; CURRENT FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/800, 929

; PRIOR FILING DATE: 1997-02-13

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO: 8

; LENGTH: 618

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-617-053A-8

Query Match 6.3%; Score 462; DB 4; Length 618;

Best Local Similarity 26.0%; Pred. No. 2.1e-33;

Matches 155; Conservative 82; Mismatches 214; Indels 146; Gaps 22;

QY ::::::::::::::::::::: 38 LEEBEBQKERAKMOKGYNQNSMRSEAKRUKFTVYEPYSWIP -- OEMAAAGFTGVWSG 94

Db 28 LSDWTNSNKKMKYDFSC -- LYRMSTYSTFPGPVPSERSLARAGFYTGNDK 80

QY ::::::::::::::::::::: 95 IOCFCCSLILFGAGLTRPIEDHKRFHPCGF -- LLNLDVGNIAKDYIRVKN ----- 144

Db 81 VKCFCGMLMDWKWKGSPPIQRKOLQPLPSCFQNLYASLSLGSFSKNTSPMRNSFAHSLS 140





## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,929A

FILING DATE: 13 FEB 1997

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 60/030,590

FILING DATE: 14-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bleier-Brady, Kristina

REGISTRATION NUMBER:

TELECOMMUNICATION/DOCKET NUMBER: 07891/009001

TELEPHONE: 617-428-7045

TELEFAX: 617-428-0200

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-800,929A-14

## Query Match

Best Local Similarity 6.3%; Score 457.5; DB 4;

Length 612; Matches 148; Conservative 73; Mismatches 207; Indels 129; Gaps 19;

OY 43 QKERAQKMQG--YNSOMRSEAK-----RLKFVTWEPYSSWIP--QEMAAAGSYFT 89

Db 16 QKURIMKESTLISNWTKESEKKMFDFSCELYRMSTYSAFPGPVYERSLARAGFYT 75

OY 90 GVKSGIQCFCCLSLILFGAGLTRLPIEDHFRFHDCGFF--LINKDVONIAKYDIRVKNLK 145

Db 76 GNDKVVKFCGCCMLDNWKOGDSVPEKHQFYPLSCSFVOTLLSASLQSPK--NMSPVK 132

QY 147 SRU-----RG-----KMRQQEELARLASFRNPFWYQ 174

Db 133 SRFHASSPLERGGIHSNLCSPLNSRAVEDFSSRMPCSYAMSTEARLTYSWMP--LS 190

OY 175 GISPVLSEAGFVFTKGDKDPTVOCFGCGCLGNWEEDDPPWKEHAKWPKCEFLRSKSE 234

Db 191 FLSPAELARAGFYVIGPDRVACFGCKLSNWPEPKDAMSEHRRHFPCHPFLENSETQ 250

OY 235 EIQYIQSFKGFVDITGEHFVNSWVORELPMASACNDSTFAVELRLRUDSKFDPRESAV 294

Db 251 RFS-----ISNLSMOPHHSARLRTFLYWPSPV 278

QY 295 GVALKAGLAGFTTGKDIVOCFGCGCLEKWKQEDDPDLDTRICFPNCPFLQNMMAEV 354

Db 279 QPEQLASAGFYVDRNDVKKFCGCCDGGLRKWEPDPDWIEHAKWPKCEFLRMMGQ-EF 337

QY 355 TPDLSR-GENCCELETTSENLSNLDIAVGPVTPPEMAQGEAQWFEQAKNLNEOLRAYTS 413

Db 338 VDECIQARYPHILEULLSTDTPGHEADPTTVHCPGE-----KMRQQEELARLASFRNPFWYQ 174

QY 414 ASFRIMSLADDISOLATDHLGCDLSTASKHTSKPQEPPLVPEWFGNLNSVMV---E 469

Db 380 KDVVNMTSTVKAAL-----MGRFSRSLVRQTVROI--LATGENVRYNTDIVSLVNLNE 432

QY 470 GEAGSGKTVLKKTAELWLWASGCCPLNRFQVLYV-SLSSTRPDEGLASTICDQLEKEGS 529

Db 433 DERREK--EIQTEEMASGDLSLIRKNMALFOQLTIVLP-----ILDNL-EAS 480

QY 530 VTERCMRNIIOQLKQV 545

Db 481 VTKQEHDIRO-KTQI496

RESULT 12

US-08-569-749-14

Sequence 14, Application US/08569749

PATENT NO. 610757

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

ATTORNEY: Goeddel, David V

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLIER, HOHBACH, TEST, ALBRITTON &amp; HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749

FILING DATE: 08/08/2002

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.

REGISTRATION NUMBER: 24-774

TELECOMMUNICATION/DOCKET NUMBER: A-62464/DJB

TELEPHONE: (415)398-3249

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 612 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-569-749-14

## Query Match

Best Local Similarity 6.3%; Score 457.5; DB 4;

Length 612; Matches 148; Conservative 73; Mismatches 207; Indels 129; Gaps 19;

OY 43 QKERAQKMQG--YNSOMRSEAK-----RLKFVTWEPYSSWIP--QEMAAAGSYFT 89

Db 16 QKURIMKESTLISNWTKESEKKMFDFSCELYRMSTYSAFPGPVYERSLARAGFYT 75

OY 90 GVKSGIQCFCCLSLILFGAGLTRLPIEDHFRFHDCGFF--LINKDVONIAKYDIRVKNLK 145

Db 76 GNDKVVKFCGCCMLDNWKOGDSVPEKHQFYPLSCSFVOTLLSASLQSPK--NMSPVK 132

QY 147 SRU-----RG-----KMRQQEELARLASFRNPFWYQ 174

Db 133 SRFHASSPLERGGIHSNLCSPLNSRAVEDFSSRMPCSYAMSTEARLTYSWMP--LS 190

OY 175 GISPVLSEAGFVFTKGDKDPTVOCFGCGCLGNWEEDDPPWKEHAKWPKCEFLRSKSE 234

Db 191 FLSPAELARAGFYVIGPDRVACFGCKLSNWPEPKDAMSEHRRHFPCHPFLENSETQ 250

QY 355 TPDLSR-GENCCELETTSENLSNLDIAVGPVTPPEMAQGEAQWFEQAKNLNEOLRAYTS 413

Db 338 VDECIQARYPHILEULLSTDTPGHEADPTTVHCPGE-----KMRQQEELARLASFRNPFWYQ 174

QY 414 ASFRIMSLADDISOLATDHLGCDLSTASKHTSKPQEPPLVPEWFGNLNSVMV---E 469

Db 380 KDVVNMTSTVKAAL-----MGRFSRSLVRQTVROI--LATGENVRYNTDIVSLVNLNE 432

QY 470 GEAGSGKTVLKKTAELWLWASGCCPLNRFQVLYV-SLSSTRPDEGLASTICDQLEKEGS 529

Db 433 DERREK--EIQTEEMASGDLSLIRKNMALFOQLTIVLP-----ILDNL-EAS 480

QY 530 VTERCMRNIIOQLKQV 545

Db 481 VTKQEHDIRO-KTQI496

RESULT 12

US-08-569-749-14

Sequence 14, Application US/08569749

PATENT NO. 610757

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

ATTORNEY: Goeddel, David V

## Query Match

Best Local Similarity 6.3%; Score 457.5; DB 4;

Length 612; Matches 148; Conservative 73; Mismatches 207; Indels 129; Gaps 19;

OY 43 QKERAQKMQG--YNSOMRSEAK-----RLKFVTWEPYSSWIP--QEMAAAGSYFT 89

Db 16 QKURIMKESTLISNWTKESEKKMFDFSCELYRMSTYSAFPGPVYERSLARAGFYT 75

OY 90 GVKSGIQCFCCLSLILFGAGLTRLPIEDHFRFHDCGFF--LINKDVONIAKYDIRVKNLK 145

Db 76 GNDKVVKFCGCCMLDNWKOGDSVPEKHQFYPLSCSFVOTLLSASLQSPK--NMSPVK 132

QY 147 SRU-----RG-----KMRQQEELARLASFRNPFWYQ 174

Db 133 SRFHASSPLERGGIHSNLCSPLNSRAVEDFSSRMPCSYAMSTEARLTYSWMP--LS 190

OY 175 GISPVLSEAGFVFTKGDKDPTVOCFGCGCLGNWEEDDPPWKEHAKWPKCEFLRSKSE 234

Db 191 FLSPAELARAGFYVIGPDRVACFGCKLSNWPEPKDAMSEHRRHFPCHPFLENSETQ 250

QY 355 TPDLSR-GENCCELETTSENLSNLDIAVGPVTPPEMAQGEAQWFEQAKNLNEOLRAYTS 413

Db 338 VDECIQARYPHILEULLSTDTPGHEADPTTVHCPGE-----KMRQQEELARLASFRNPFWYQ 174

QY 414 ASFRIMSLADDISOLATDHLGCDLSTASKHTSKPQEPPLVPEWFGNLNSVMV---E 469

Db 380 KDVVNMTSTVKAAL-----MGRFSRSLVRQTVROI--LATGENVRYNTDIVSLVNLNE 432

QY 470 GEAGSGKTVLKKTAELWLWASGCCPLNRFQVLYV-SLSSTRPDEGLASTICDQLEKEGS 529

Db 433 DERREK--EIQTEEMASGDLSLIRKNMALFOQLTIVLP-----ILDNL-EAS 480

QY 530 VTERCMRNIIOQLKQV 545

Qy 355 TPDLSR-GEIcellettssnledsiavgvpiVPEMAQGAEAQWFOEAKNLNEQLRAATS 413  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 338 VDEIQARYPHILEQOLISTDPGEENADPTEVWHRGPGE-----SS 379  
 Qy 414 ASFRIMSLDSSDIATDHJLGCDISIASKHISKVPOEPIVLPVEFGNLSVMCV---E 469  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 380 EDVVMKSTPVKALE---MGFSRSLVROTVOROI--LATGENYRTVNDIVSVLNAE 432  
 Qy 470 GEAGSCKTVLKKIAFLWASGCCPLNRFQLVFYLSLSSTRPDEGLASITCDOLEKEGS 529  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 433 DERREK--ERQEEMASGDSLJRKNMALQOLTHWR----ILDNLU-EAS 480  
 Qy 530 VTEMCMRNNTIOQLKNQY 546  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 481 VTKQEHDIRQ-KTOI 496

RESULT 13  
 US-09-617-053A-14  
 ; Sequence 14, Application US/09617053A  
 ; Patent No. 6300492  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kornejuk, Robert G  
 ; APPLICANT: Mackenzie, Alexander E  
 ; APPLICANT: Liston, Peter  
 ; APPLICANT: Baird, Stephen  
 ; APPLICANT: Tsang, Benjamin K  
 ; APPLICANT: Pratt, Christine  
 ; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
 ; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
 ; DISEASE  
 ; FILE REFERENCE: 07891/00903  
 ; CURRENT APPLICATION NUMBER: US/09/617, 053A  
 ; CURRENT FILING DATE: 2000-07-14  
 ; PRIORITY NUMBER: US 08/800,929  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO: 14  
 ; LENGTH: 612  
 ; TYPE: PRT  
 ; ORGANISM: MUS musculus  
 ; US-09-617-053A-14

Query Match 6.3%; Score 457.5; DB 4; Length 612;  
 Best Local Similarity 26.6%; Pred. No. 5.3e-33; Mismatches 207; Indels 129; Gaps 19;  
 Matches 148; Conservative 73; Mismatches 207; Indels 129; Gaps 19;

Qy 43 OKERAKMOKG--YNSQMRSEAK----RLKTFVTEPYVSSWIP--QEMAAAGFYFT 89  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 16 OKLKRIMEKSTILSNNTKESBEKMKDFDSCLYRMSYSAFPRGVFVSESLARAGFYT 75  
 Qy 90 GVKGJOCFCSSILFGAGLTPLIDHKRPHDGF--LINKVGNTIAYDIRVKNL 146  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 76 GVDKVRFCFCGMLMDWKQODSPVKEHQFPCPSFVQTULASLQSPSK--NMSPVK 132  
 Qy 147 SRL-----RGG-----KMRQEEERLASFRNWFYVQ 174  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 133 SRFANHSPLERGGIHNLCSSPLNSRAVEDFSSRMDCSTAMSTEERAFUTYSMP--LS 190  
 Qy 175 GISPCVULSEAGFVFTRQKQDTVQCFSCGGCLGNWEECDDPWNKHEAKWFPKCEFFLRKSSE 234  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 191 FLSPLAELARAGFYYIGPGDRVACFACGGKLNSWEPKDAMSEHRRHFPCHPFLENSETQ 250  
 Qy 235 ETI TOY OTOS YKFVFDITRGEHFVNWSWQRELPMASAYCNDSITAYEELDLERFKWHRRESA 294  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 251 RFS-----TSNLSMQTHSARLRTFLYWPSPV 278  
 Qy 295 GVAALAKAGLTYTGKDIWOCFFCGGLEKWMQEGDPLDDTRCFNCPELQNMKSAEV 354  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 279 QPEQLASAGFVYVDRNDVKCCDGGLRCWPGDDPWIEHAKWFPCEFLIRMKG-EF 337

RESULT 14  
 PCT-US96-12860-14  
 ; Sequence 14, Application PC/US9612860  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TULARIK, INC.  
 ; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT  
 ; STREET: 4 Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US96/12860  
 ; FILING DATE: 06 AUG 1996  
 ; CLASSIFICATION:  
 ; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Breezer, David J  
 ; REGISTRATION NUMBER: 24,774  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 81-1989  
 ; TELEFAX: (415) 398-3249  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 612 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; PCT-US96-12860-14

Query Match 6.3%; Score 457.5; DB 5; Length 612;  
 Best Local Similarity 26.6%; Pred. No. 5.3e-33; Mismatches 207; Indels 129; Gaps 19;  
 Matches 148; Conservative 73; Mismatches 207; Indels 129; Gaps 19;

Qy 43 OKERAKMOKG--YNSQMRSEAK----RLKTFVTEPYVSSWIP--QEMAAAGFYFT 89  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 16 OKLKRIMEKSTILSNNTKESBEKMKDFDSCLYRMSYSAFPRGVFVSESLARAGFYT 75  
 Qy 90 GVKGJOCFCSSILFGAGLTPLIDHKRPHDGF--LINKVGNTIAYDIRVKNL 146  
 ; ::-|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 76 GVDKVRFCFCGMLMDWKQODSPVKEHQFPCPSFVQTULASLQSPSK--NMSPVK 132

RESULTS

Db 133 SFAHSSPLERGIGHSNLCSPLNSRAVEDFSSRMDPCSASYMSSTEARRLTYSWP--LS 190 QY 175 GSPCVSLEAGAVFTGHQDWTQFCSCGGCGNWEKGDDPKHEAKWPRCEFRSKSE 234 Db 191 FUSPLAARAFYVIGPDRVACFGKLUSNWEPKDDAMSEURHFFHCPLLENSETQ 250 QY 235 ETOYIQSYKGFVDITGEHFVNWSWQRELPMASACNCISI-FAYEELRUDSKDWRESAV 294 Db 251 RFS-----ISNMSPHSANLRTFLWPPSVV 278 QY 295 GVALAKAGLFYTGKDIVOCFSGGCLEKWAEGDDPBDHRCFPNCPCFQNMSSAEV 354 Db 279 OPEQLASAGFYVYDRNDVKFCFCDDGLRCWEPGRGDPDKHEAKWPRCEFLRMKGQ-EF 337 QY 355 TPDQSR-GELCELETTSESNELDSTAVGPVPEMAQGEAQWFOEAKNLNEQLRAAYS 413 Db 33B VDEOQARYPHILQOLSLSTDPEGENADPTEWHRGPE -----SS 379 QY 414 ASFRIMSLIDDISSLDATDHLLGCDLSIASKHTSKPQVEPVLPEVFGNLNSVMCY--E 469 Db 380 EDVMMSTPVVKALE---NGFSRSLVQVQROI---LATGENVRTNDIVSLLNAE 432 QY 470 GEAGSKVLUKKIAFLWASGCCPLNRFLQVFLSLSSTRPDEGLASLICDOLLEKGS 529 Db 433 DERREEK--EROTEEMA-ASGDSLRLKRKNMALLEQOLTLWLP-----ILDNL--EAS 480 QY 530 VTEMCMNITIQLKNOV 546 Db 481 VTKQEHDIQ-RKTOI 496

RESULT 15

US-09-212-971-12

; Sequence 12, Application US/09212971B

; General Information:

; Applicant: Korneluk, Robert G

; Applicant: Liston, Alexander E

; Applicant: Linton, Peter

; Applicant: Baird, Stephen

; Applicant: Tsang, Benjamin K

; Applicant: Pratt, Christine

; Title of Invention: DETECTION AND MODULATION OF IAPS AND TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE TITLE OF INVENTION: DISEASE

; File Reference: 07891/009002

; Current Application Number: US/09/212-971B

; Current Filing Date: 1998-12-16

; Earlier Application Number: 60/017, 354

; Earlier Filing Date: 1996-04-26

; Earlier Application Number: 60/030, 590

; Earlier Application Number: 1996-11-14

; Earlier Filing Date: 1997-02-13

; Software: FastSEQ for Windows Version 4.0

; SEO ID: NO 12

; Length: 600

; Type: PRT

ORGANISM: Mus musculus

SEARCHED BY: SIS-09-212-971-12

SEARCHED ON: September 30, 2002, 15:04:59

SEARCH TIME: 245 sec

SEARCHED BY: SIS-09-212-971-12

SEARCHED ON: September 30, 2002, 15:04:59

SEARCH TIME: 245 sec

RESULTS

Db 126 SENTGYFSSYSSFPSPDNFRANQDCPALSTSPYHFMNTKEARLYETWP--LSFLS 183 QY 178 PCVUSEAGAVFTGHQDWTQFCSCGGCGNWEKGDDPKHEAKWPRCEFLRSKSSEIT 237 Db 184 PAKLAQAYYTGDRVACFGKLUSNWEPKDDAMSEURHFFHCPLLENSETQ 356 QY 238 QYIOSYKGFVDITGEHFVNWSWQRELPMASACNCISI-FAYEELRUDSKDWRESAV 296 Db 240 -----ASRYTVSNMTHAIRTFSNWSLLNHS 271 QY 297 AALAKAGLFYTGKDIVOCFSGGCLEKWAEGDDPBDHRCFPNCPCFQNMSSAEV 356 Db 272 QELASAGFYVYDRNDVKFCFCDDGLRCWEPGRGDPDKHEAKWPRCEFLRMKGQ-EF 331 QY 357 DLQSGELCELETTSESNELDSTAVGPVPEMAQGEAQWFOEAKNLNEQLRAAYS 400 Db 332 VOAGYHPLLEOLSLSTDPEGENADPTEWHRGPE -----SS 379 QY 401 --KNLNEQRKA--YTSASFRIIMSLIDDISSL-----ATDHLIGCDSIASHKISK 447 Db 391 LVRQTVQROQLATGENRTVSDLVIGLDAEDEMRESCMQEAEEESDDALIRNNMV 450 QY 448 PVQE-PLVPEVEFNLSYMCVEAGGKTVLUKFLWASGCCPLNRFQFLYFLSL 505 Db 451 LFQHITCVPMLYCILSARAITEOCNAVK-----480 QY 507 SSTRDEGLASITCDOLEKEGVTECMRNTIQQLKNOV--LFULLDYK----EIGS 558 Db 481 --QKPHTQASTLTDVTVAK-GNTAATSFRIISREDPALYRDIVQODRSLPDDINA 537 QY 559 IP--QVICKLKLONHLSFTCL 577 Db 538 LPMEEOIKRL-OBERMCKVM 557